Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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US-08-296-749-2	US-08-475-680-2	US-08-863-790-2	US-08-714-017-2	US-08-720-420A-2	US-08-483-932-2	US-08-473-503-2	US-08-487-595-4	US-08-487-113D-2	US-08-483-389-2	US-08-485-604-4	US-08-482-882-2	US-08-656-984A-4	US-08-481-130-4	US-08-245-295-4	US-08-433-010-2	US-08-314-362-2	US-08-314-615-2
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TELEFA SEQUENCE LENGTH TYPE: STRAND TOPOLO MOLECULE FEATURE: NAME/K LOCATI -121-321	APPLI FILIN CLASS IOR A APPLI FILIN TORNE TORNE REGIS REGIS REFER REFER	-09-121-32 Sequence 1 Sequence 1 Sequence 1 APPLICA AP	_
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TELEFAX: INFORMATION F SEQUENCE CH LENGTH: LENGTH: TYPE: nu STRANDEDM TOPOLOGY: MOLECULE TY FEATURE: PATURE: LOCATION: US-09-121-321-15	APPLICATIO FILING DAT CLASSIFICA CLASSIFICA CLAS APPLICATIO FILING DAT TORNEY/AGE TORNEY/AGE NAME: Hall REGISTRATI REGISTRATI LECOMMUNIC TELEPHONE:	21-321-15 APPLICANT: PPLICANT: PRENT APPLICANT: PRENT APPLICANT: REAMEDITME: REAMEDI	
நென்ற இர	APPLICATION NUMBER: US/ FILING DATE: CLASSIFICATION: PRIOR APPLICATION DATA: APPLICATION UNMBER: US/ ETLING DATE: 19-SEP-199 ATTORNEY/AGENT INFORMATION NAME: Haltey, James F. REGISTRATION NUMBER: 27- REGISTRATION NUMBER: TELECOMMUNICATION INFORMAT TELECOMMUNICATION INFORMAT TELECOMMUNICATION INFORMAT	Sequence 15, Application US/09121321 Sequence 15, Applicant Saiga, Akihiko APPLICANT: Saiga, Akihiko APPLICANT: Igarashi, Hisanaga APPLICANT: Igarashi, Gaku TITLE OF INVENTION: GENE EXPRESS INVENTION: GENE EXPRESS OCORRESPONDENCE ADDRESS: ADDRESSEE: FISH & NEAVE STREET: 1251 Avenue of the Ame CITY: New York COUNTRY: USA ZIP: 10020 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DO SOFTWARE: Datentin Release #1. CURRENT APPLICATION DATA:	
212-596-9090 BR SEQ ID NO: RACTERISTICS: RACTERISTICS: 777 base pairs Leic acid SS: double linear E: cDNA CDS 1392151	PICE TO NE	System Control of Parent In Parent I	
-596- EQ ID ITERIST base base doul near cDNA		licat TION: TION: rita, garras kumur NTION NTION NTION NTION NTION NTION NTION NTION TION	
ID NO RESTRICT NO	NUMBER: US/09/1 ION: TION DATA: NUMBER: US 08/9 19-SEP-1997 INFORMATION: James F. VJames SHOOLO	NICATION US/09121 183 183 17ION: AIGA, Akihiko 184 194 184 184 184 184 184 184 184 184 184 18	
9090 NO: TICS Pai Dai	TA: : U : U : U : U : EP-1 MATI MATI MATI MATI MATI MATI MATI MATI	on US/0 Akihiko Satoshi Satoshi , Kouic hi, Kouic hi, GeNE CONA M CENE 20 ESS: 6 NEAVE nue of PC-DO In Rel-DATA:	
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15:	US/09/121,321 US 08/933,803 1997 ION: 27,794 ER: SHGN-12C	idhiko itioshi Hisanaga Kouichi Oak MOLECULE I DNA MOLECULE I DNA MOLECULE I E of the Ameri Release #1.0, ATA: Release #1.0,	
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US-08-933-803A-15
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                                                                                                       Query Match 3.6%;
Best Local Similarity 83.6%;
                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Haley, James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
                                                                                                                                                                                                                                                                                                      TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Saiga, Akihiko
APPLICANT: Orita, Satoshi
APPLICANT: Igarashi, Hisanaga
APPLICANT: Okumura, Kouichi
APPLICANT: Sakaguchi, Gaku
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: DNA MOLECULE RELATING TO SUPPRESSION OF TITLE OF INVENTION: GENE EXPRESSION AND NOVEL PROTEIN NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                            CORRESPONDENCE ADDRESS
 1462 aaaaaaaaaaaaa 1474
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Local Similarity 83.6%;
nes 61; Conservatino
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                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: 139
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                                                                                                                                                                                                                                                                              TYPE:
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DEDNESS: double
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SYSTEM: PC-DOS/MS-DOS
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                                                                                          Score 53.8; DB 4;
Pred. No. 2e-05;
Pred. No. 2e-12;
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                                                                                                                        DB 4; Length 3777;
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RESULT 4
US-08-606-505B-1
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                                                                                                                                                                                                                     Query Match

Best Local Similarity 71.0%;
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INFORMATION FOR SEQ ID NO:
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                                                                                   1442 aaaaaaaaaaaaaaaaaaaaaaaaaaaaa 1474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Perkins, Patricia Anne REGISTRATION NUMBER: 34,695 REFERENCE/DOCKET NUMBER: 2827 TELECOMMUNICATION INFORMATION: TELEPHONE: 206-587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/236,919
FILING DATE: 06-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.1
SOCTWARE: Microsoft Word for Apple, Version :
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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APPLICANT: Giri, Judith G
                                                                                                                                                           1382 tttgtatotgaacatotggcccatcgtacattcagtaaagcctataatagcgggcaaaaa 1441
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1641 base pairs
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ATTORNEY/AGENT INFORMATION:
                                                                     1559 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1591
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 Mismatches

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; Sequence 1, Application US/08605505B ; Patent No. 6114601 ; GENERAL INFORMATION:

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US-09-616-990-1
; Sequence 1, Application US/09616990
; Patent No. 6232109
; GENERAL INFORMATION:
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Best Local Similarity 60.8%;
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                                                                                                                                                                                                                                                                  1345 agagaagtaaatacaacagaacaggctaatatagtgttttgtatctggaacatctggccca 1404
                                                                                                                                                  1465 aaaaaaaaaa 1474
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                                                                                                                                                                                      1695 AAAGGAGTACATGAAGCGCATTGCATGAGTTTAACTTGTAGCTCCTTAATATTTTTAGGTA 1754
                                                                                                                                  1815 AAAAAAAAA 1824
                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1824 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Perry Lawrence S.
REGISTRATION NUMBER: 31865
TELECOMMUNICATION INFORMATION: TELEPHONE: 212-218-2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.50 inch, 720 Kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: JP44963/92
FILING DATE: '02-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: SHIMADA, Ritsuko
APPLICANT: OKINAKA, Yasushi
TITLE OF INVENTION: NOVEL PLANT GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                  IDENTIFICATION METHOD: by experiment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN: Falcon Blue
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              APPLICANT: KIKUCHI, Yasuhiro
                                                                                                                                                                                                                                                                                                                 79;
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KIYOKAWA, Shigeto
SHIMADA, Yukihisa
OHBAYASHI, Masaya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Petunia hybrida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FITZPATRICK, CELLA, HARPER & SCINTO
KIYOKAWA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA to mRNA
                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                     Score 48.4; DB 3;
Pred. No. 0.00045;
                                                                                                                                                                                                                                                                                                                                      Length 1824;
                                                                                                                                                                                                                                                                                                            Indels
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RESULT 6
US-08-757-046A-5
US-08-757-046A-5
Sequence 5, Application US/08757046A
Patent No. 5876995
GEMERAL INFORMATION:
APPLICANT: Bryan, Bruce
TITLE OF INVENTION: BIOLUMINESCENT
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; SEQUENCE DESCRIPTION: SEQ ID NO: 1 US-09-616-990-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 3.3%; Score 48.4; DB 4; Length 1824; Best Local Similarity 60.8%; Pred. No. 0.00045;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1345 agagaagtaaatacaacagaacaggctaatatagtgttttgtatctgaacatctggccca 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 1 : SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                        1815 AAAAAAAAA 1824
                                                                                                                                                                                                                                                                                             1465 aaaaaaaaaa 1474
                                                                                                                                                                                                                                                                                                                                  1695 AAAGGAGTACATGAAGCGCATTGCATGAGTTTAACTTGTAGCTCCTTAATATTTTAGGTA 1754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAMÉ: Perry, Lawrence S.
REGISTRATION NUMBER: 31865
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-218-2100
TELEFAX: 212-218-2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: MS-DOS Ver3:30
SOFTWARE: PATENT AID Ver1.0
CURRENT APPLICATION DATA:
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COUNTRY: U.S.A.
ZIP: 10112-3801
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.50 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 02-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 14-Jul-2000 PRIOR APPLICATION DATA:
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OKINAKA, Yasushi
TITLE OF INVENTION: NOVEL PLANT GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79;
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LOCATION:
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LOCATION: 116 to 1633
IDENTIFICATION METHOD: by experiment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Petunia hybrida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1824 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: JP44963/92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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OHBAYASHI, Masaya
                                              BIOLUMINESCENT ARTICLES OF MANUFACTURE 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                       US-09-447-208-5
                                                                                                     RESULT
                                                      Sequence 5, Application US/09447208 Patent No. 6113886
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                                                                                                                                                                                                                                                                                               Query Match
            GENERAL INFORMATION:
APPLICANT: Bryan, Bruce
TITLE OF INVENTION: BIO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6680-105B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US
FILING DATE: 11-25-96
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COMPUTER READABLE FORM:
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PRIOR APPLICATION DATA:
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                                                                                                                                                             NAME/KEY: Coding Sequence LOCATION: 115...702
OTHER INFORMATION: apoaeque PUBLICATION INFORMATION:
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LENGTH: 958 base pairs
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NUMBER OF SEQUENCES:
                                                                                                                                              COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                         DATE: (1985)
DOCUMENT NUMBER: PATENT NO.: 5,093,240
                                                                                                                                                                                                                                                                                                                                                                                  PAGES: 3154-3158
                                                                                                                                                                                                                                                                                                                                                                                                     VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 619-238-0062
                                                                                                                                                                                                                                                                 Local Similarity les 67; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS:
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              BIOLUMINESCENT ARTICLES OF
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Pred. No. 0.00047;
0; Mismatches 32;
                                                                                                                                                                                                                                                                      32;
                                                                                                                                                                                                                                                                                                    Length 958;
                  MANUFACTURE
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; VOLUME: 82
; PAGES: 3154-3158
; DATE: (1985)
US-09-447-208-5
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Best Local :
                                                                                                                 Matches
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SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Seldman, Stephanie L
REGISTION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0
FILING DATE: 02-06-96
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PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US/09/447, 208
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HYPOTHETICAL: NO
ANTI-SENSE: NO
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               1376 tagtgttttgtatctgaacatctggcccatcgtacattcagtaaagcctataatagcggg 1435
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                                                                                                                                                                                                                                                                           PUBLICATION INFORMATION: PATENT NO.: 5,093,240
                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                  FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
                                                       TELEPHONE: bir ... TELEPHONE: bir ... 619-450-8499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 08-17-
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                                                                                                                 Local Similarity hes 67; Conserv
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                 JOURNAL:
                                                                                                                                                                                                                                                               AUTHORS:
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                                                                                                                                                                                                                                                                                                                      NAME/KEY: Coding Sequence LOCATION: 115...702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE:
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                                                                                                                 Conservative
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                                                                                                                                Score 47.8; DB 3; Pred. No. 0.00047;
                                                                                                                    Mismatches
                                                                                                                                                 DB 3;
                                                                                                                     32;
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US-09-135-988-5
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                                                                                           Matches
                                                                                                                      Query Match
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                                           1376 tagtgttttgtatctgaacatctggcccatcgtacattcagtaaagcctataatagcggg 1435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NFORMATION FOR SEQ ID NO:
NAME/KEY: Coding Sequence LOCATION: 115...702
OTHER INFORMATION: apoaeque PUBLICATION INFORMATION:
                        PUBLICATION INFORMATION: PATENT NO.: 5,093,240
                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 619-450-8400
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                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL: N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 958 base pairs
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FILING DATE: 02-06-96
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                      AUTHORS:
JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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                                                                                                     Local
                                                                                                                                                                                                           VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 0: FILING DATE: 11-25-96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/135,988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
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                                                                                         l Similarity
67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid
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                                                                                         Conservative
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                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                    Inouye et al.
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67.7%;
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                                                                                               Score 47.8; DB 3; Length 958; Pred. No. 0.00047;
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                                                                                    Mismatches
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RESULT 10
US-08-597-274A-5
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; Sequence 5, Application US/09277716A
; Patent No. 6232107
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                                                                                                                                                                                  Sequence 5, Application US/08597274A Patent No. 6247995
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PUBLICATION INFORMATION:
PATENT DOCUMENT NUMBER: 5,093,240
PATENT FILING DATE: 1987-10-08
PATENT FILING DATE: 1992-03-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                  GENERAL INFORMATION:
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VOLUME: 82(10)
PAGES: 3154-3158
DATE: 1985-05
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EARLIER APPLICATION NUMBER: 60/102,939
EARLIER FILING DATE: 1998-10-01
EARLIER APPLICATION NUMBER: 60/089,367
EARLIER FILING DATE: 1998-06-15
EARLIER FILING DATE: 1998-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bryan, Bruce
APPLICANT: Szent-Gyorgyi, Christopher
APPLICANT: PROLUME, LTD.
TITLE OF INVENTION: LUCIFERASES, FLUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE CURRENT APPLICATION NUMBER: US/09/277,716A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS: Inouye, S.
TITLE: Cloning and sequence analysis of cDNA for the luminescent protein JOURNAL: Proc. Natl. Acad. Sci. USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 958
TYPE: DNA
ORGANISM: Aequorea (luminescent jellyfish)
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NAME/KEY: CDS
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                                                                                      NUMBER OF SEQUENCES: I
                                                                                                                                                  APPLICANT:
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                                                                                                                               TITLE OF INVENTION:
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CITY: San Diego
STATE: CA
 COUNTRY:
                                                                      ADDRESSEE:
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                                                1660 Union Street
USA
                                                                                                                                               Bryan, Bruce
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                                                                      Brown, Martin, Haller & McClain
                                                                                                                           BIOLUMINESCENT NOVELTY ITEMS
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DATE: (1985)
US-08-597-274A-5
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Best Local :
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: 19-238-0999
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
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LOCATION: 115...702
OTHER INFORMATION: apoaequ
PUBLICATION INFORMATION:
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TITLE OF INVENTION: Mannanase enzymes, genes coding for them,
TITLE OF INVENTION: methods for isolating the genes, and methods for bleaching lighted for invention: pulps
                                                   APPLICANT: Viikari, Liisa
APPLICANT: Penttila, Merja
APPLICANT: Saloheimo, Anu
APPLICANT: Marjatta, Ranua
                                                                                                                  APPLICANT: Buchert, Johanna APPLICANT: Siika-aho, Matti
                                                                                                                                                                                                                                                                     AUTHORS:
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REFERENCE/DOCKET NUMBER: 6680-105
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REGISTRATION NUMBER: 33,771
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                                                                                                                                                                                                                                                                                                                                                                                                                        Match 3.2%; Score 47.8; DB 4; Length 958; Local Similarity 67.7%; Pred. No. 0.00047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOCUMENT NUMBER: 5,093,240 AUTHORS: Inouye et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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                                                                                   Siika-aho, Matti
Viikari, Liisa
Penttila, Merja
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Murphy Jr, Gerald M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 36
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 536 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Saloheimo, Anu APPLICANT: Marjatta, Ranua RITLE OF INVENTION: Mannanase enzymes, genes coding for them, TITLE OF INVENTION: methods for isolating the genes, and methoristic of INVENTION: lignocellulosic pulps
                                                                                                NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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CITY: Falls Church
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/341,568
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COUNTRY: US
ZIP: 22040-0747
                                 STATE:
                                               STREET: PO Box 747 CITY: Falls Church
                                                                                  ADDRESSEE:
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                                                                E: Birch, Stewart, Kolasch and Birch
PO Box 747
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Siika-aho, Matti
                                                                                                                                                                                                                                   Viikari, Liisa
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Pred. No. 0.00057;
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                                                                                                                                                      and methods for bleaching
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US-08-911-020-1
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Best Local (
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APPLICATION NUMBER: US 08/341
PRIOR NOTE: 22-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: MUTPHY JT, Gerald M
REGISTRATION NUMBER: 28,977
REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 248345
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 536 base pairs
                                                          OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
                                                                                                                                              ZIP: 94304
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Yue, Henry
TITLE OF INVENTION: CAF1-RELATE
                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: cDNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
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                                APPLICATION NUMBER: FILING DATE: Filed
                                                                                                                    COMPUTER:
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                 CLASSIFICATION:
                                                                                                                                                                                                              CITY: Palo Alto
                                                                                                                              MEDIUM TYPE: Diskette
                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                              ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/0 FILING DATE: 13-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
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                                                                                                                                                                                                CA
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                                                                                                           IBM Compatible
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SYSTEM: PC-DOS/MS-DOS
                                Filed Herewith
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ON: CAF1-RELATED PROTEIN
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                                              US/09/027,137
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RESULT 14
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IMMEDIATE SOURCE:
LIBRARY: PROSNO
CLONE: 2229466
                                                                        FILING DATE: 17-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Silveri, Jean M.
                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                            TELECOMMUNICATION INFORMATION:
                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/715,032
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
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                                           REFERENCE/DOCKET NUMBER: MN
                                                                                                                                                                          FILING DATE:
             TELEPHONE:
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REGISTRATION NUMBER: 36,749
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STRANDEDNESS: single
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: (617)227-7400
(617)227-5941
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/ENTION: Weight Control Pathway Genes and Uses
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; TOPOLOGY: 1i
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US-08-897-340-1
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Patent No. 6147192
GENERAL INFORMATION:
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                                        Query Match 3.2%; Score 46.6; DB 3; Length 1386; Best Local Similarity 64.6%; Pred. No. 0.0012; Matches 64; Conservative 3; Mismatches 32; Indels 0
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SEQUENCE CHARACTERISTICS:
LENGTH: 1386 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                       TELEFAX: (617)227-5941 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: Silveri, Jean M.
REGISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER: MNI-
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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LENGTH: 1386 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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MEDIUM TYPE: Floppy disk
1376 tagtgttttgtatctgaacatctggcccatcgtacattcagtaaagcctataatagcggg 1435
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APPLICATION NUMBER:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Gimeno, Carlos J. and Errada, Patrick, R. TITLE OF INVENTION: Weight Control Pathway Genes and Uses TITLE OF INVENTION: Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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Search completed: October 2, 2001, 05:48:56 Job time: 3226 sec

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DB seq length: 2000000000
A_Geneseq_0601:*

//SIDSB/gcgdata/geneseq/geneseqp/AA1980.DAT:*
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Maximum Match 100%
Listing first 45 summaries
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1 1530 100.0 294 22 AAY71974 Maize RAD5 2 1530 100.0 294 22 AAY71976 Maize RAD5 3 1450 94.8 281 22 AAY71975 Maize RAD5 4 576.5 37.7 376 21 AAY73340 HTRM clone 5 324 21.2 350 21 AAY91937 Alali3 mod 6 323 21.1 350 19 AAW56264 Human reco 7 323 21.1 350 19 AAW56265 9 313 20.5 350 19 AAW56265 10 300 19.6 286 21 AAC43526 Murine Rec 11 300 19.6 344 21 AAG43526 Zea mays p	SUMMARIES  Result Query No. Score Match Length DB ID  Description
Maize RAD51 orthol Maize RAD51 orthol Maize RAD51 orthol HTRM clone 2398682 Ala163 modified hu Human recombinase Human Rec2 serine Mouse recombinase Murine Rec2 serine Zea mays protein f Zea mays protein f	scription

Protein involved i Thermus aquaticus	AAY36888 AAR93198	20 17	487 340	6.1	94 93.5	5
	AAY81563	21	764		95	Ω.
⊆ .	AAY81751	21	763	6. 2	95	2 =
Zea mays keca-like Arabidonsis thalia	AAY44386	18	1 38 A		97.5	- 6
pidopsis	AAG28750	21	198	•	97.5	39
٦	AAW44138	19	347	6.6	101	8
Helicobacter pylor	AAW44140	19	273		101	37
Deduced sequence o	AAR79145	16	273		101	8
Protein involved i	AAY37531	20	386	6.7	103	Ğ
Bacteriophage Dp-1	AAB16691	21	386		104	4
$\sim$	AAR29636	13	451	٠	107	ω
ВS	AAY34339	20	462	7.4	113.5	2
Porphorymonas ging	AAY34463	20	461	•	113.5	ũ
Recombinase enzyme	AAW01871	17	781	8.2	126	ö
Arabidopsis thalia	AAG44430	21	128		137.5	9
	AAG44429	21	159	10.0	153	8
Arabidopsis thalia	AAG44428	21	189		200	27
DNA replication an	AAY82743	21	346		243	6
ZmRAD51A amino aci	AAY42375	20	340	17.7	271.5	
Fission yeast RAD5	AAR78182	16	365	18.0	276	4
Glycine max RAD51	AAY72086	22	344	18.2	278.5	ü
Wheat RAD51 recomb	AAY72088	22	343	18.3	279.5	2
ad51	AAY87917	21	339	18.3	280.5	ï
Sequence of the sp	AAW62522	19	339	•	280.5	õ
Mouse RAD51 protei	AAR78181	16	339		280.5	6
3	AAR54070	15	339		0	ω
Human Rad51 protei	AAY87918	21	339		_	7
Sequence of the sp	AAW62523	19	339		81	9
Human RAD51 protei	AAR78183	16	339	18.4	281.5	5
ZmRAD51B amino aci	AAY42376	20	340	18.5	83	4
MC1 pr	30	19	344		299	ω
Zea mays protein f	AAG43525	21	372	19.6	300	ึง

4333333332222222222222

## ALIGNMENTS

AAY71974 RESULT

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AAY71974 standard;

Protein;

294 AA

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New maize RAD51 polynucleotides, useful for e.g. controlling recombination or transformation efficiency in plants, or as pamplification primers for detecting, quantifying or isolating
                                                                                                                                                                                                                                    Maize; RAD51 orthologue; RAD52 epistasis group; double strand break; DSB; homologous recombination; transformation; gene targetting; transgenic plant; DNA repair.
                                            WPI; 2001-016092/02.
N-PSDB; AAD02118.
                                                                                                                                                                                                                                                                                 Maize RAD51 orthologue protein
                                                                                                                                                                                                                                                                                                                              AAY71974;
                                                                                                                          05-MAY-1999;
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                                                                                                                                                                     16-NOV-2000.
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                                                                                                                                                                                                                 Zea mays.
                                                                                                                                                                                                                                                                                                        28-MAR-2001
                                                                              Mahajan PB,
                                                                                                  (PION-) PIONEER HI-BRED INT INC.
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probes or gene

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RESULT
AAY71976
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
05-MAY-1999;
                                 05-APR-2000; 2000WO-US09010.
                                                                                                    WO200068370-A2
                                                                                                                                                                  Maize; RAD51 orthologue; RAD52 epistasis group; double str
homologous recombination; transformation; gene targetting;
transgenic plant; DNA repair.
                                                                   16-NOV-2000
                                                                                                                                                                                                                                        Maize RAD51 orthologue protein
                                                                                                                                                                                                                                                                                                                                              AAY71976 standard; Protein; 294 AA
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Local Similarity 100.0%;
hes 294; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hirq diedlal rtrvlsglslkl mkiaktynlavvll nqvttk ftegsfqltlalgdsws
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSHEKSSSVQKQLQPERFLADIYYFRICSYTEQIAVINYMEKFLREHKDVRIVIIDSVTF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VPGVGKTQLGIQLAINVQIPVECGGLGGKAVYIDTEGSFMVERVYQIAEGCIRDILEHFP 120
                                                                                                                                                                                                                                                                                                                                                                                                                           hsctnrlilh wngnery ahldk spslpvas apyavtgkgird avssnhkrarvt\\
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                294 AA;
                                                                                                                                                                                                                                                                          (first entry)
99US-0132582
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Pred. No. 3.3e-157;
0; Mismatches 0;
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3
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(PION-) PIONEER HI-BRED INT INC.

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Mahajan PB, Shi J;

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MPI; 2001-016092/02.

DR

NPSDB; AAD02120.

XY

New maize RAD51 polynucleotides, useful for e.g. controlling recombination or transformation efficiency in plants, or as probes or primers for detecting, quantifying or isolating gene recombination primers for detecting, quantifying or isolating gene primarscripts

XX

Claim 1; Page 74-75; 76pp; English.

XX

The present sequence is a maize RAD51 orthologue protein #3. RAD51 is one of the genes of the RAD52 epistasis group that is involved in double control of the genes of the RAD52 epistasis group that is involved in double control of the genes of the repeater by homologous recombination. Control of the genes of the repeater by homologous recombination of incollection primers for detecting the repeater by homologous recombination of incollection gene targetting in transgenic plants. The RAD51 control of the major isolating gene transcripts, in detecting plants. The RAD51 control of the major isolating gene transcripts, in detecting defliciencies in control gene mutations, for monitoring upregulation of expression or confidence in enzyme activity, for detecting any number of allelic variants, concluded polypeptide, or for use as immunogen in preparing and/or its encoded polypeptide, or for use as immunogen in preparing and/or concreasing of antibodies, and in sense or antisense suppression of one or used in assays to agonise or antagonise the enzyme function, or as immunogens or antigens to obtain antibodies.

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Sequence 294 AA;
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Query Match
Best Local
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 241
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                                                                                                                             HSHEKSSSVQKQLQPERFLADIYYFRICSYTEQIAVINYMEKFLREHKDVRIVIIDSVTF
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                            HSCTNRLILHWNGNERYAHLDKSPSLPVASAPYAVTGKGIRDAVSSNHKRARVT
                                                       hfrqdfedlalrtrvlsglslklmkiaktynlavvllnqvttkftegsfqltlalgdsws
                                                                                                              hsheksssvqkqlqperfladiyyfricsyteqiavinymekflrehkdvriviidsvtf
                                                                                                                                                                     vpgvgktqlgiqlainvqipvecgglggkavyidtegsfmvervyqiaegcirdilehfp
                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                  100.0%; Score 1530; DB 22; 100.0%; Pred. No. 3.3e-157; tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                              Length 294;
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RESULT AAY71975

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AAY71975 standard; Protein; 281 AA

24 24 25 27 27 27 27

DX AX DX DX AX B

28-MAR-2001

(first entry)

Maize RAD51 orthologue protein

Maize; RAD51 orthologue; RAD52 epistasis group; double strand break; homologous recombination; transformation; gene targetting;

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                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is a maize RAD51 orthologue protein #2. RAD51 is one cof the genes of the RAD52 epistasis group that is involved in double strand breaks (DSBs) repair by homologous recombination. Control of homologous recombination by modulating RAD51 is used for improving transformation and gene targetting in transgenic plants. The RAD51 control of nucleotide may be used as probes or amplification primers for detecting, cquantifying or isolating gene transcripts, in detecting deficiencies in the mRNA level during screening for desired transgenic plants, for cdetecting gene mutations, for monitoring upregulation of expression or contrologues or paralogues of the gene, or for site directed mutagenesis in eukaryotic cells. It may also be used for recombinant expression of convergenes in a host cell, tissue or plant. The RAD51 proteins may be used in assays to agonise or antisones suppression of one or more genes in a host cell, tissue or plant. The RAD51 proteins may be
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New maize RAD51 polynucleotides, useful for e.g. controlling recombination or transformation efficiency in plants, or as paramplification primers for detecting, quantifying or isolating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PION-) PIONEER HI-BRED INT INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunogens or antigens to obtain antibodies.
 239
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               HSCTNRLILHWNGNERYAHLDKSPSLPVASAPYAVTGKGIRD 282
                                                                                                                                                                                                                                                                                      MGDQSGSRNGPQQKYVSGAQNAWDMFSDELSQKHITTGSGDLNDILGGGIHCKEVTEIGG
                                                                                                                                                     HSHEKSSSVQKQLQPERFLADIYYFRICSYTEQIAVINYMEKFLREHKDVRIVIIDSVTF 180
                                                                                                                                                                                                                                      VPGVGKTQLGIQLAINVQIPVECGGLGGKAVYIDTEGSFMVERVYQIAEGCIRDILEHFP 120
hsctnrlilhwngneryahldkspslpvasapyavtgkgird
                                                                                               HFRQDFEDLALRTRVLSGLSLKLMKIAKTYNLAVVLLNQVTTKFTEGSFQLTLALGDSWS 240
                                                                                                                                                                                                    vpgvgktqlgiqlainvqipvecgglggkavyi--egsfmvervyqiaegcirdilehfp 118
                                                                                                                                                                                                                                                                    mgdqsgsrngpqqkyvsgaqnawdmfsdelsqkhittgsgdlndilgggihckevteigg 60
                                                               hfrqdfedlalrtrvlsglslklmkiaktynlavvllnqvttkftegsfqltlalgdsws
                                                                                                                                   hsheksssvqkqlqperfladiyyfricsyteqiavinymekflrehkdvriviidsvtf 178
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                                                                                                                                                                                                                                                                                                                                                           94.8%;
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                                                                                                                                                                                                                                                                                                                                                          Score 1450; DB 22; Pred. No. 1.4e-148;
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AAY73340
ID AAY7
  leukaemia; immune disorders such as AIDS, Addison's disease, diabetes mellitus, rheumatoid arthritis, multiple sclerosis, systemic lupus erythematosus, and myasthenia gravis; infections and trauma. Antagonists of the HTRM polypeptides are useful for treating or preventing disorders associated with increased expression or activity of HTRMs. HTRM polypeptides, their immunogenic fragments or oligopeptides are useful polypeptides, their immunogenic fragments or oligopeptides are useful for screening libraries of compounds in drug screening techniques. Polypucleotides encoding HTRM are useful for blocking the transcription of mRNA and regulating gene function by modulating the activity of HTRM. Vectors expressing HTRM or agonists can also be used to prevent or treat disorder associated with decreased HTRM expression. Antibodies
                                which specifically bind HTRN and polynucleotides encoding HTRN are useful for diagnosing disorders associated with the expression of HTRN. particularly in assays that detect the expression of HTRN. Nucleotide sequences encoding HTRN may be useful to generate hybridization probes useful in mapping the naturally occurring genomic sequence and to detect differences in gene sequences among normal, carrier and affected individuals. Using diagnostic assays, cancer can be detected prior to the appearance of clinical symptoms and thereby progression of cancer can be prevented by aggressive treatment or preventive measures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein sequences. The HTRM protein and nucleotide sequences are userul for preventing or treating disorders associated with decreased expression or activity of HTRM which include cell proliferative disorders such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY73325-Y73389 are human transcriptional regulator molecule (HTRM) protein sequences. The HTRM protein and nucleotide sequences are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1;
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02-OCT-1998;
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Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arteriosclerosis and cirrhosis; cancers including adenocarcinoma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAZ52425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Addison's disease; multiple sclerosis; rheumatoid arthritis; infection; trauma; myasthenia gravis; adenocarcinoma; immune disorder; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HTRM clone 2398682 protein sequence
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  376 AA;
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98US-0102745
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Azimzai Y,
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Lu DAM;
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Qy

Matches Query Match Best Local

125;

Conservative

47;

Similarity

37.78; 43.98;

Score 576.5; DB 2 Pred. No. 7.4e-54; Mismatches

DB 21;

Length 376;

Indels

15;

Gaps

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RESULT
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                    The present sequence is Ala163 hsRec2, a human serine kinase modified a Y163A substitution. The hsRec2 is in the same supergene family as t mammmalian protein having homologous pairing and strand transfer activities, RAD51 and was isolated because of its homology to the homologous pairing and strand transfer protein of Ustilago maydis. In particular, hsRec2 phosphorylates several proteins that control the ce cycle, especially cyclin E and p53. The invention permits the phosphorylation of cell cycle control proteins at sites that are physiologically relevant. The invention can be practiced with either murine or human Rec2 or a mutein or chimera of these proteins. In
                                                                                                                                                                                                                                                                                                                                                                                                           Phosphorylating a serine-containing substrate by incubating it adenosine triphosphate and Rec2 kinase and measuring the level phosphorylation, useful for discovering specific antagonists of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYJE-) UNIV JEFFERSON THOMAS (CORR ) CORNELL RES FOUND INC (KIME-) KIMERAGEN INC.
                                                                                                                                                                                                                                                                                                                                 Claim 18; Page -; 41pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 324; DB 21;
Pred. No. 1.4e-26;
O; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
                                                                                                                                                                                                                            sequence'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48;
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11-SEP-1997;

97WO-IB01217

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Best Local :
Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATP-dependent recombinase of Ustilago maydis (USREC2). Its amino acid sequence was deduced from cDNA clones (see AAV22703) isolated on the basis of homology to UmREC2. Overexpression of mammalian REC2 (see also AAW56265) in a cell facilitates homologous recombination between an exogenous DNA and the genome of a cell It also sensitises the cell to DNA damage, e.g. by gamma or UV radiation or from cytotoxic agents. This causes the cell to undergo apoptosis in response to DNA damage. The haracz gene can be used in gene therapy protocols and in a method for constitution of the cell to DNA damage.
                   Homo sapiens
                                       phosphorylation;
                                                                      Human Rec2 serine kinase.
                                                                                                                                     AAY91932 standard; Protein; 350 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  be used in gene therapy protocols and in a method for classifying human tissue for medical purposes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This polypeptide comprises the human homologue, HSREC2, of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 5; Fig 1A-B; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalian and human REC2 genes encoding - useful for the sensitisation of cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Holloman WK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-SEP-1996;
                                                                                                                                                                                                                                                                                                  143
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                                                                                                                                                                                                                                                                             188
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                                                                                                                                                            7
                                                                                                                                                                                                           GDSWSHSCTNRLILHWNGNERYAHL-DKSPSLPVASAPYAVTGKGI
                                                                                                                                                                                                                                                                           vlqriesleeeii---
                                                                                                                                                                                       gntwshsvntrlilgyldserrqiliaksplapftsfvytikeegl 342
                                                                                                                                                                                                                                  reasslkylaeefsipviltnqitthlsgalasqadlvspaddlslsegtsgsscviaal
                                                                                                                                                                                                                                                        GLSLKLMKIAKTYNLAVVLLNQVTTKF-----
                                                                                                                                                                                                                                                                                              YYFRICSYTEQIAVINYMEKFLREHKDVRIVIIDSVTFHFRQDFE-----DLALRTRVLS
                                                                                                                                                                                                                                                                                                                    egavvyidtesafsaerlveiae-----srfpryfnteekllltsskvhlyreltcde
                                                                                                                                                                                                                                                                                                                                         GGKAVYIDTEGSFMVERVYQIAEGCIRDILEHFP---HSHEKSSSVQKQLQPERFL-ADI 142
                                                                                                                                                                                                                                                                                                                                                             sadfspaflsttlsaldealhggvacgslteitgppgcgktqfcimmsilatlptnmggl 134
                                                                                                                                                                                                                                                                                                                                                                                    SDELSQKHITTGSGDLNDILGGGIHCKEVTEIGGVPGVGKTQLGIQLAINVQIPVECGGL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1998-207378/18.
                                      serine kinase; homologous
rylation; cyclin E; p53; ce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORNELL RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                               350 AA;
                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JEFFERSON THOMAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kmiec EB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96US-0025929
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                   21.1%; 32.2%;
                                                                                                                                                                                                                                                                         ·-----skgiklvildsvasvvrkefdaqlqgnlkernkfla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rice MC,
                                                                                                                                                                                                                                                                                                                                                                                                           44;
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 323; DB 19;
Pred. No. 1.8e-26;
                                      us pairing; strand transfer;
cell cycle.
                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP-dependent recombinase(s) to the apoptotic effects of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Smith
                                                                                                                                                                                                                                                                                                                                                                                                          100;
                                                                                                                                                                                                                                                      -----TEGSFQLTLAL
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 350;
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                                                 RAD51;
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                                   Qγ
                                                         В
                                                                             QΥ
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Best Local :
                                                                                                                                              Matches
                                                                                                                                                                                                 Sequence
                188
                                     143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Havre PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
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murine or human Rec2 or a mutchin or chimera of these proteins. In particular the mutch has the sequence of a Rec2 kinase containing other than a Tyr at position 163. The invention comprises a method of phosphorylating a serine-containing substrate comprising incubating the substrate with ATP (adenosine triphosphate) and Rec2 kinase or a mammalian Rec2 and measuring the level of phosphorylation. The method is useful for discovering compounds which are specific antagonists or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the same supergene family as the mammmalian protein having homologous pairing and strand transfer activities, RAD51 and was isolated because of its homology to the homologous pairing and strand transfer protein of Ustilago maydis. In particular, hsRec2 phosphorylates several proteins that control the cell cycle, especially cyclin E and p53. The invention permits the phosphorylation of cell cycle control proteins at sites that are physiologically relevant. The invention can be practiced with either marries by homes poor or marries of the proteins at sites that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phosphorylating a serine-containing substrate by incubating it with adenosine triphosphate and Rec2 kinase and measuring the level of phosphorylation, useful for discovering specific antagonists or agonists of Rec2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              agonists of Rec2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 18; Page 33-34; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYJE-) UNIV JEFFERSON THOMAS (CORR ) CORNELL RES FOUND INC (KIME-) KIMERAGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAA08553.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-283562/24.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present sequence is the hsRec2, a human serine kinase.
                                                                                                                                                                                                                                                                                                                                                              SDELSQKHITTGSGDLNDILGGGIHCKEVTEIGGVPGVGKTQLGIQLAINVQIPVECGGL 86
                                                             vlqriesleeeii-----skgiklvildsvasvvrkefdaqlqgnlkernkfla
                                                                                                                           YYFRICSYTEQIAVINYMEKFLREHKDVRIVIIDSVTFHFRQDFE-----DLALRTRVLS 197
                                                                                                                                                                                             egavvyidtesafsaerlveiae-----srfpryfnteekllltsskvhlyreltcde
                                                                                                                                                                                                                                                           GGKAVYIDTEGSFMVERVYQIAEGCIRDILEHFP---HSHEKSSSVQKQLQPERFL-ADI 142
                                                                                                                                                                                                                                                                                                                        sadfspaflsttlsaldealhggvacgslteitgppgcgktqfcimmsilatlptnmggl 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rice MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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163
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160..163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= B_Box_motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186..199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "preferaby any amino acid other than
    tyrosine in the claimed method"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= nuclear_localization_signal 108..116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21.1%; 32.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Holloman WK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "src-type phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                               44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 323; DB 21;
Pred. No. 1.8e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 350;
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TEGSFQLTLAL
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                                                                                                              Qγ
                                                                                                                                                                                                                                             recombination between an exogenous DNA and the genome of a cell. It also sensitises the cell to DNA damage, e.g. by gamma or UV radiation or from cytotoxic agents. This causes the cell to undergo apoptosis in response to DNA damage. The muREC2 gene can used in the construction of transgenic animals and knock-out mice useful as models for tumorigenesis induced by chemical pathogens.
                                                                                                                                                                                                                                                                                                                                     This polypeptide comprises the murine homologue, muREC2, of the ATP-dependent recombinase of Ustilago maydis (USREC2). Its amino acid sequence was deduced from a cDNA clone (see AAV2704) isolated on the basis of homology to UmREC2. Overexpression of mammalian REC2 (see also AAW56264) in a cell facilitates homologous
                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 1E-F; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalian and human REC2 genes encoding - useful for the sensitisation of cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-MAR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse recombinase muREC2 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-AUG-1998 (first entry)
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                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAV22704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Holloman WK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinase; REC2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       irradiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         237 reasslkylaeefsipviltngitthlsgalasgadlvspaddlslsegtsgsscviaal
   130 Q--KQLQPERFLADIYYFRICSYTEQIAVINYMEKFLREHKDVRIVIIDSVTFHFRQDFE 187
                            125 atlptslgglegavvyidtesaftaerlveiae-----srfpqyfnteekllltssrv
                                                           77
                                                                                    65 qtayelktrrsahlspaflsttlcaldealhggvpcgslteltgppgcgktqfcimmsvl 124
                                                                                                                20 QNAWDM---FSDELSQKHITTGSGDLNDILGGGIHCKEVTEIGGVPGVGKTQLGIQLAIN 76
                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gntwshsvntrlilqyldserrqiliaksplapftsfvytikeegl 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1998-207378/18
                                                      VQIPVECGGLGGKAVYIDTEGSFMVERVYQIAEGCIRDILEHFP---HSHEK----SSSV 129
                                                                                                                                               100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UNIV JEFFERSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer;
                                                                                                                                                                                                                      350 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kmiec EB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96US-0025929
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RES FOUND INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hsREC2; homologous recombination; irradiation;
                                                                                                                                                              20.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THOMAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rice MC,
                                                                                                                                               46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       350
                                                                                                                                                              Score 313; DB 19;
Pred. No. 2.2e-25;
                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATP-dependent recombinase(s) to the apoptotic effects of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smith
                                                                                                                                                 98;
                                                                                                                                                                            Length 350;
                                                                                                                                                 Indels
                                                                                                                                                 68;
                                                                                                                                                 Gaps
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                                 177
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                                                                                     The present sequence is the muRec2, a murine serine kinase. It is in the same supergene family as the mammmalian protein having homologous pairing and strand transfer activities, RADS1 and was isolated because of its homology to the homologous pairing and strand transfer protein of its homology in particular, muRec2 phosphorylates several proteins ustilago maydis. In particular, muRec2 phosphorylates several proteins that control the cell cycle, especially cyclin E and p53. The invention permits the phosphorylation of cell cycle control proteins at sites that are physiologically relevant. The invention can be practiced with either are physiologically relevant.
murine or human Rec2 or a mutein or chimera of these proteins. In particular the mutein has the sequence of a Rec2 kinase containing other than a Tyr at position 163. The invention comprises a method of phosphorylating a serine-containing substrate comprising incubating the substrate with ATP (adenosine triphosphate) and Rec2 kinase or a
                                                                                                                                                                                                                                                                                                  phosphorylating a serine-containing substrate by incubating it with adenosine triphosphate and Rec2 kinase and measuring the level of phosphorylation, useful for discovering specific antagonists or agonists of Rec2
                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-283562/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYJE-) UNIV JEFFERSON THOMAS (CORR ) CORNELL RES FOUND INC (KIME-) KIMERAGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-SEP-1998;
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phosphorylation; cyclin E; p53; cell cycle.
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                                                                                                                                                                                                                                                               Disclosure; Page 34-36; 41pp; English
                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
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tyrosine in the claimed method"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                      mays subsp. mays.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pklqgnikernkflgkgasl-lkylagefsipviltnqitthlsgalpsqadlvspaddl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VQIPVECGGLGGKAVYIDTEGSFMVERVYQIAEGCIRDILEHFP---HSHEK----SSSV 129
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Pred. No. 2.2e-25;
6; Mismatches 98; Indels 6
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RESULT 11
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hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence; corn.
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                                                                                                                     Zea mays subsp. mays.
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88; Conservative
                                                                                                                                                                                                                               standard; Protein;
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                                                                2000EP-0301439
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41; Mismatches
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                                                  Zea mays subsp. mays.
                                                                        termination sequence;
                                                                                Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                  Zea mays protein fragment SEQ ID NO: 54413.
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       AtDMC1 protein sequence
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16-AUG-1999; 17-AUG-1999; 13-AUG-1999; 13-AUG-1999; 10-AUG-1999; 11-AUG-1999;

12-AUG-1999;

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 AAY42376
                                  AAY42376 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated Arabidopsis meiosis-specific promoter - useful meiosis-specific transcription of genes, e.g. for isolation apomictic plants or removing DNA from transgenic plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana meisosis-specific DMCl gene; AtDMCl; promoter; meiosis specific expression; ablation; meiotic cell; isolation; appomictic plant; increase; meiotic recombination; introgresssion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                  Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This is the amino acid sequence of the ZmRAD51B recombinase enzyme. The RAD51 recombinase from 5. cerevisiae has a role in the catalysis of the in vitro pairing and strand exchange between circular viral single strand DNA and linear duplex DNA. The identification of the ZmRAD51 genes will allow the identification and characterisation of
                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 8; Page 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Maize recombinase genes ZmRAD51A and ZmRAD51B useful targeting system and production of transgenic plants
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expression vector; plasmid;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-AUG-1999.
246 RLILH-WNGNERYAHLDKSPSLPVASAPYAVTGKGIRD
                                                                                                                                                                                146
                                              240 sarqmhlakflrslqkladefgvavvitnqvvaqvdgaamfagpqikpiggnimahastt
                                                                                190
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                                                                                                                                                                                                                                                                               18 GAQNAWDMFSDELSQKHITTGSGDLNDILGGGIHCKEVTEIGGVPGVGKTQLGIQLAINV 77
                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1999-527374/44.
DB; AAZ11870.
                                                                                ALRTRVLSGLSLKLMKIAKTYNLAVVLLNQVTTKFTEGSF----QLTLALGDSWSHSCTN
                                                                                                                                                                               qlpldqgggegkalyidaegtfrpqrilqiadrfglnga--dvlenvayarayntdhqsr
                                                                                                                                                                                                                                              gftsasqlhaqrleiiqlttgsreldqildggietgsitemygefrsgktqlchtlcvtc 145
                                                                                                                                                LQPERFLADIYYFRICSYTEQIAVINYMEKFLREHKDVRIVIIDSVTFHFRQDFE----DL
                                                                                                                                                                                                 QIPVECGGLGGKAVYIDTEGSFMVERVYQIAE-----GCIRDILEHFPHSHEKSSSVQKQ
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                                                                                                                                                                                                                                                                                                                                                                                              340 AA;
                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene targeting; gene insertion; transgenic plant;
ector; plasmid; meiosis-specific homologue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66pp; English
                                                                                                                                                                                                                                                                                                                             18.5%;
                                                                                                             -aasmmvetrf-----almvvdsatalyrtdfsgrgel
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                                                                                                                                                                                                                                                                                                              50;
                                                                                                                                                                                                                                                                                                                             Score 283.5;
Pred. No. 3.
                                                                                                                                                                                                                                                                                                              Mismatches
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for gene

Indels Length

Gaps

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340; 39;

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300 rlflrkgrgeerickvisspclaeaearfqissegvtd 337

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AAR78183
ID AAR781
                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                              DNA coding for a RAD51 protein having the amino acid sequence in AR78183 is claimed. The RAD51 protein, which contains an ATP-binding domain, is involved in DNA repair of mismatched base pairs and site-specific recombination in antibody gene rearrangements. The protein binds to double-stranded DNA to form a right-handed helical nucleoprotein that extends (by 1.5 times) the pitch of B-form DNA. As a result, the helix is unwound. The RAD51 protein will be useful in designing drugs to treat diseases associated with environmental DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Structural gene encoding RAD51, used in production of RAD51 - used to study drugs against diseases caused by DNA damage, e.g. by UV or x radiation, and to improve efficiency of gene therapy targetting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 16-17; 19pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1995-236467/31.
N-PSDB; AAQ91763.
261 DKSPSLPVASAPYAVTGKGIRDA 283
                                     | : :|||: ||| : :|:
| 256 adefgvavvitnqvvaq-vdgaamfaadpkkpiggniiahasttrlylrkgrgetricki 314
                                                                         207 AKTYNLAVVLLNQVTTKFTEGSFQLTL-----ALGDSWSHSCTNRLILH-WNGNERYAHL 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TOYM ) TOYOBO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-MAY-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA mismatch repair; DNA recombination; site-specific; unwinding; right-handed helical nucleoprotein; RAD51; human; recA;
                                                                                                                                      150 YTEQIAVINYMEKFLREHKDVRIVIIDSVTFHFRQDFE---DLALRTRVLSGLSLKLMKI 206
                                                                                                                                                                                                                         topoisomerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human RAD51 protein, involved in DNA repair.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR78183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR78183 standard; Protein; 339 AA.
                                                                                                                                                                                                     95 TEGSFMVERVYQIAE-----GCIRDILEHFPHSHEKSSSVQKQLQPERFLADIYYFRICS 149
                                                                                                                                                                                                                                                                            35
                                                                                                                                                                                                                                                                                                         Local Similarity 30.4 es 80; Conservative
                                                                                                         -----yqasammvesryallivdsatalyrtdysgrgelsarqmhlarflrmllrl 255
                                                                                                                                                                    tegtfrperllavaeryglsg--sdvldnvayarafntdhqtqll------ 204
                                                                                                                                                                                                                                                                  ITTGSGDLNDILGGGIHCKEVTEIGGVPGVGKTQLGIQLAINVQIPVECGGLGGKAVYID 94
                                                                                                                                                                                                                                                                                                                                                                                       339 AA;
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                                                                                                                                                                                                                                                                                                    18.4%; Score 281.5; DB 16; Length 339; 30.4%; Pred. No. 5.4e-22; 7ative 46; Mismatches 96; Indels 41;
                                                                                                                                                                                                                                                                                                    Indels 41; Gaps
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Db 315 ydspclpeaeamfainadgvgda 337

Search completed: October 1, 2001, 16:28:15
Job time: 48 sec

Page 14

Run

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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Sequence:
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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BC000667	AP002908	AP003310	AF029669	ATH299424	AX046603	AX046605	AX046601	ID		
BC000667 Homo sapi	AP002908 Oryza sat	AP003310 Oryza sat	AF029669 Homo sapi	AJ299424 Arabidops	AX046603 Sequence	AX046605 Sequence	AX046601 Sequence	Description		

Gaps

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RESULT 1
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                                                                                                                                                                                                              AUTHORS
TITLE
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nays
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
                                                                                                                                                                                                                            Mahajan, P.B. and Shi, J.
                                                                                                                                                                                                                                        Panicoideae; Andropogoneae;
1 (bases 1 to 1474)
                                                                                                                                                                                       PIONEER HI-BRED
                                                                                                                                                                               from maize
t: WO 0068370-A 1 16-NOV-2000;
ER HI-BRED INTERNATIONAL, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'n
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AC029940 Giardia i
AC078679 Giardia i
AC078679 Giardia i
AF079428 Zea mays
AX047126 Sequence
AF079429 Zea mays
AX047126 Jeam Gardia i
U43528 Arabidopsis
AX047122 Sequence
AF017729 Oryctolag
M87549 Saccharomyc
D10865 Yeast genes
U18922 Saccharomyc
AB026115 Pyrobacul
AC045789 Giardia i
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AF052597 Pyrococcu
AL407915 T3 end of
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AC011195 Homo sapi
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U22441 Lycopersico
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ILGGGIHCKEVTEIGGVPGVGKTQLGIQLAINVQIPVECGGLGGAVINVIEGSFWVERV
YQIAEGCIRDILEHFPHSHEKSSSVQKQLQFERFLADIYYFRICSYTEQIAVINVMEK
ELREHKDVRIVIIDSVTFHFRQDFEDLALRTRVLSGLSLKLMKLAKTYNLAVVLLNQV
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                                                            ggttctggtgacctcaatgacatacttggtggcgggattcactgcaaagaagttactgag 480
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                                                                                                                                                                                                                                                                                                                                               /translation="MISFGRRKSPAIEETSLATSVMEAWRLPLSPSIRGKLISAGYTG LSSIASVSSSDLARDANITEEEAFEILKLANGSCONGSRSLINGKNAMDMLHEEESL PRITTSCSDLDNILGGGISCNDVTEIGGVPGIGKTQIGIOLSVNVQIPEEGGLIGKA IYIDTBGSFMVKRALQIAEAGVDMEEXTGYMIKHFQANQVQMKPEDILENIFYFRVC SYTEQIALVHILEKFISENKDYKVVIYDSITHHFQOYDDLAQRTRULSEMALKFMKL
                                                                                                                                                                                                                                                                                                                       AKKFSLAVVLLNQVTTKFSEGSFQLALALGDSWSHSCTNRVILYWNGDERYAYIDKSP
SLPSASASYTVTSRGLRNSSSSSKRVKMM"
                                                                                                                                                                                                                                                                                                                                                                                                                      /product="RAD51C protein"
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/db_xref="GI:10944745"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Arabidopsis thaliana"
/cultivar="Columbia"
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V Homo sapiens Rad51C (R

AF029669

AF029669.1 GI:2000000
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                                                                                                       Submitted (09-OCT-1997) Life Sciences, Laboratory, Ms. 70A-1118, Berkeley, CA
                                                                                                                                  Schild,D., Collins,D.W. and Dosanjh,M.K.
Direct Submission
                                                                                                                                                                                                                                      Shen, Z. and Schild, D.
                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                              98136197
                                                                                                                                                                                                                                                                                                                           human
                                                                                                                                                               (bases 1 to 1295)
                                  /chromosome="17"
                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                         Location/Qualifiers
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cactttccgcacagccatgagaagtcctcttctgtccaaaaacaattacagcctgagcgt 720
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Dosanjh,M.K., Collins,D.W., Fan,W., Lennon,G.G., Albala,J.S.,
                                                                                                                                                                                                                                                                                                                                                                                                           Isolation and characterization of RAD51C, a RAD51 family of related genes
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/map="17g; 413.6cR from the top"
/cell_type="leukocyte (mixed pop
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(RAD51C) mRNA, complete
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                                       tgattctgcactggaatgggaacgaacgatacgcacatcttgataagtctccttcacttc 1108
                                                                                                                 ATCAGGCCTTGCTTCCTGCATTAGGGGAAAGTTGGGGGACATGCTGCTACAATACGGC
                                                                                                                                     ggtcatttcaattgactcttgctctaggttgacagctggtcccactcatgcacgaaccggt 1048
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ELSKEVGISKAEALETLGIIRRECLTNRPRYAGTSESHKKCTALELLEGEHTQGFIIT
FCSALDDILGGGVPLKKTTEIGGAPGVGKTOLLMQLAVDVQIPECFGGVAGBAVFIDT
EGSFMUDRVULATACIQHAQIA TEKKKGEHRKALEDFTLDNILSHIYFFGRDYTE
LLAQVYLLPDFLSEHSKVRLYTVDGIAFPFRHDIDDLSLRTRLINGLAQQMISLANNH
RLAVILTNQMTTKIDRNQALLVPALGESWGHAATIRLIFHWDRKQRLATLYKSPSQKE
RLAVILTNQMTTKIDRNQALLVPALGESWGHAATIRLIFHWDRKQRLATLYKSPSQKE
CTVLFQIKPGGFRDTVVTSAGSLGTBGSLSTRKRSRDPEEEL"

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43. .1173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="RAD51C"
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Pred. No. 1.5e-32;
0; Mismatches 361
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Query Match
Best Local Similarity
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gtatagttattattgatagtgttactttccacttt
                                                                               CTGAACAAATTGCAGTCATAAACTATCTGGAAAAGTTTCTTGGGGAGCATAAAGATGTAA 2398
                                                                                                                                                                                                                       aacaattacagcctgagcgtttcctggcggatatctattacttccggatatgcagttaca 760
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                                                                                                                                                                                           AAAAACTGAAGCCTGAGAGTTTCCTGGCTGACATCTACTACTTCGAATATGCAGCTATA
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NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This sequence will be replaced

* This sequence will be replaced

* This sequence will be replaced
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Sasaki,T., Matsumoto,T. and Yamamoto,K.
Direct Submission
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Pred. No. 1.2e-30;
0; Mismatches 65
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SEQUENCING IN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rel:81-298-38-7441, Fax:81-298-38-7468)
On Feb 28, 2001 this sequence version replaced gi:11136550.
Genes were predicted from the integrated results of the following:
GENSCANI.0, BLASTN2.0, BLASTN2.0 as well as SplicePredictor
(October 1998 version). The genomic sequence was searched against
NCBI NORREDUNGANT PROTEIN ACTABLES, nr
(ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at
RGP. Protein homologies of the coding regions were searched against
NCBI NORREDUNGANT PROTEIN ACTABLES.

NCBI NORREDUNGANT PROTEIN ACTABLES.

The identified cDNA sequences using BLASTN2.0. ESTS represent
the identified cDNA sequences using BLASTN2.0 with the
corresponding DDBJ accession no. and RGP clone ID.
A gene with identity or significant homology to a protein is
classified based on the protein name to indicate the homology level
such as same name, 'putative-' and '.like protein'. A gene without
significant homology to any protein but with EST homology (covering
'unknown' protein. A gene predicted with a gene prediction program
is classified as a 'hypothetical' protein.

The orientation of the sequence is from T7 to SP6 of the PAC clone.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://rgp.dna.affrc.go.jp/GenomeSeq.html.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detailed information on overlap and assembly quality together with annotation of this entry is available at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (08-NOV-2000) Takuji Sasaki, National Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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/gene="p0013G02.1"
complement(join(2332. .2436,2786. .2871,3194.
/gene="p0013G02.1"
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                             complement(9637. .12886)
/gene="P0013G02.2"
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/gene="P0013G02.2"
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/note="3' LTR"
                                                                                                                                                                                                                 /protein_id="BAB32926.1"
/db_xref="GI:13161335"
/translation="MDLAKGYYTSPPTRCGEGEDSSLWELEMRRMWRRGGLLPVGVGD
EEEKKPGRTASYLEGVNRHI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Oryza sativa"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
/chromosome="1"
/note="probably inactive
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         CDS
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                             complement(join(47103..47281,49010.
50114..50340,50420..50490,50561..5
51241..51345,51594..51705))
/gene="P0013G02.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="BAB32929.1"
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GOMplement(join(31561..32021,32574..33461,33560..33820,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="BAB32927.1"
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GMCIVLGYPHGVDYQGKKLPEQDGDDAEPHAAWEVTAVILTGSPERTSLAVTAGGDSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGGGAARVDLDGGAPAIGELDEGVDGVDGCAAKPEEATPGREAVSEEPNVVNRITTAF
WELQLPACSDEPISSGTPSSPSSPPTKETGDANTVVIDDLFLAHSDAILPAGGDQKEE
HQLGDDLGQQQAATAMEIDDDVIYSLIRNWDNDSSSSWIELLDHAIVSPASCFVPWKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(15279. .16871)
/note="5' LTR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(13135. .13944,14966. .15037))
/gene="P0013G02.3"
                                                                                                                                                                                                                                                                               LSWYRWRKQRVVAGSPAAVGGRCSTDAAGKDSFRKSASSTLVSLEYSNGWDPLADGRG
GIGFSQEVAQSFRFNMEDVESATQYFSELNILGKNGNFAATYRGTLRDGTSVVVKRLG
KTCCKQEEAEFLKGLKLLAELQHENIVGLRGFCCSRARGECFLVYDFVPNGSLSQFLD
                                                                                                                                                                                                                                                                                                                                                                         QLTGGVPTQLGLLKRLTVLELQSNHLSGAIPASLGDLPQLVRLDLSFNNLFGSIPVRL
ALLPRLLALDVRNNTLTGSVPSELAKLQGGFQYANNTDLCGTGLPALRPCTPADLISP
DMPQPFSAGISPQITPGSSSDGHGHCTGTHCPPSTKALAAVVVVAVILLAVTGAGMFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELDKEAVAGGEAAQRLLKKYVGGGGAWMNRAAGSCSIKNHVMSERRRREKLNEMFLI
LKSLVPSIDKVDKASILSETIAYLKELERRVQELESGKKVSRPAKRKPCSETIIGGGG
GGGGAGAVKEHHHWVLSESQEGTPSDVRVIVNDKDELHLEVQCRWKELMVTRVFDAIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SAACQNAALLA IGTLHQRYPDELQHSPYRYHPRRGGARDYATFWDASSEDDAT IMHLA
CMVEAYDAAR IDFHHMVRRGLVENNMK I LELRQENLQLKKDLDAVEAQLFQLK I AQGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(13135...13944,14966.
/gene="p0013G02.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similar to polyprotein'
      complement(join(47103. .47281,49010. .49076,49786. .49917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTGRLLPSWAPGRDPCGREGGGGFEGVACDGATGAVANVSLQGKGLAGTLPPAVAGLT
ALTGLYLHYNRLTGALPRELAALSRLTDLYLNVNNFSGPIPPEIAAMPSLQVVQLCYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="putative receptor-like protein kinase"
/protein_id="BAB32930.1"
/db_xref="GI:13161339"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(join(31561. 34399. .34858))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34399.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLRLDVVSVQASAPDGLLGLKIRAKYASSAAVVPAMISETLRTAVAGY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="putative transcription activator"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J∪⊥n(15203. .16463,18333.
/gene="p0013G02.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STEDVLLLTFRPGPSQK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VCHPKRRRVCRSLKITARKSTFRPELVRQSLAWTCFVETPCAEPAPVVPQEEEASGVG
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                                                                                                                                                                                       LTGKSKIMQLPLESSNDEDLIDGNLRGCYSAAEAAKLAKIASACTSENPDHRPTMEEI
                                                                                                                                                                                                                        YRPLISGSGLHKLLVDDLVFSTLKASAAMGYLAPEYTTTGRFSEKSDVYAFGVIVFQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="P0013G02.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           join(28520. .28527,29674. .29780,30119.
/gene="p0013G02.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(16203. .16463,18333.
/gene="P0013G02.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /pseudo
                                                                                                                                                                                                                                              LDADDVARSNGRVLEWSTRISIIRGIAKGIEYLHSTRANKPPLVHQNISADKVLVDYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="P0013G02.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon_start=1/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .34858)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .28527,29674.
302.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .32021,32574.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .18929,19065. .19457,20680. .20751)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .18929,19065. .19457,20680.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .29780,30119.
                                                                                                . .49076,49786.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .33461,33560. .33820,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 30294)
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Query Match
Best Local Similarity
aacaattacagcctgagcgtttcctggcggatatctattacttccggatatgcagttaca 760
                                                       GCATCAGTGATATACTGGAGTACTTTCCACACTGCCATGACAAGGCTCCAGCCGGACAAG 50230
                                                                                    gtattagggacatactggagcactttccgcacagccatgagaagtcctcttctgtccaaa 700
                                                                                                                                                           TTTTAACAGATACAGAGGGAAGTTTCATGGTTGAACGTGTCTACCAAATTGCTGAAGGGT 50290
                                                                                                                                                                                     ttatatagatacagagggcagtttcatggttgaacgtgtctaccagattgctgaagggt 640
                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement()oin(58887. .59081,60870. .61024,61113.
61319. .61416,62180. .62297,62345. .62470,62559. .(
/gene="Pol13002.9"
complement()oin(58887. .59081,60870. .61024,61113.
61319. .61416,62180. .62297,62345. .62470,62559. .(
61319. .61416,62180. .62297,62345. .62470,62559. .(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Join(53315. .53371,53419. .53458,53464. .53574,53856. .53948, 54151. .54511,54550. .54925,55256. .55423,57768. .57953)
/gene="P0013602.8"

Join(53315. .53371,53419. .53458,53464. .53574,53856. .53948,54151. .54511,54550. .54925,55256. .55423,57768. .57953)
/gene="P0013602.8"
/note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RLSPRLSWRLANLLVLGQQAKTLGASPTTELATWASHWSKMPTWPGMVLAGVTTEGQA
SWPVDDEVQRPGDGRTVVFAAFFDAGLRLLCDDFLASVLEIYEARLPQLSPSAIAKLS
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/translation="MALTSAMTSGDNGGVAGLRLDAAMPKEETVTTSEDDNGGATAHSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="BAB32932.1"
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/txns1atlon="MDPAAFIGRPIRWRRASTGDGFMLCLKAFALAFGRSSSLVVNP
LTFVARLRPRPHDKPLSLHPSGFAQVLGHGYRVYSALYCAARSDRNLLFRIPLVTLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EABEILKVANGANKSKGADGPSTSSYLKGVQNAMDMLSDEQSRRHINTGSADLNNILG
GGIHCKEVTELGGVPGVGKTQLGIQLAINVQITVEXGGJGGKAVITQTGSSFMYERVY
QIABGGISDILEXFFHCHDKAPAGQEKLKPESFLADIYYFRICSYTEQJAVLNYLEKE
LGEHKDVRIVIIDSVTFHFRQDFDDMALRTRVLSGLSLKLMKLSKAYNLAVVLLNQVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGNIWPEYMVVDETEKVSCFASCENRSELLMEQGQSEEDDMTASLMDQFEIMPQLLHY
FHYENEPDSLDWATIIVYTCKGSCDQNVSYMEBFYWYQLSPATTRTNQSTCPPAGL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QCNRSSNTIRTQN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MVLFGKLDLAGYEISTESRTICCKFFVLGIELLARNGFVRIADKKTQLAVSIQTTAFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AEMGLYIDNPYTAKYSDNAGRLRFRCLPISINSKPSMEITGLLESRLILLRNVVCRLS
THDCCEEYCMLQRTCRAGEHPCQLNNIHLFSAGDDRLATLDMTEESCLMCVLDLQLEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VRDAVNSNSKRVRVM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TKFTEGSFQLTLALGDSWSHSCTNRLILYWNGNERYGFLDKSPSLPVASAPYAVTVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="putative Rad51C protein"
/protein_id="BAB32931.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="P0013G02.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50114. .50340,50420. .50490,50561. .50594,50835. .50957, 51241. .51345,51594. .51705))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="P0013G02.10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="BAB32933.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="P0013G02.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="P0013G02.10"
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                                                                                                                                                                                                                                                                                      11.6%;
76.4%;
                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                      Score 171;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .63486,63492.
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                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                           DB 13;
                                                                                                                                                                                                                                                                                      .2e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .63811,63861.
                                                                                                                                                                                                                                                               65;
                                                                                                                                                                                                                                                                                                           Length 163419;
                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .64053)
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                                                                                                                                                                                                                                                            0,
                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3. .61203, .62774))
                                                                                                                                                                                                                                                            0,
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AUTHORS
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BC000667
  ORIGIN
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                            BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: nisc_mgc@nhgri.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Benjamin,B., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (15-NOV-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Series:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGC:2023, mRNA, complete BC000667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg,R
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IRAL Plate: 5 Row: d Column: 24.
                                                            /translation="mRGKTFRFEMQRDLVSFPLSPAVRVKLVSAGFQTAEELLEVKPS
ELSKEVGISKAEALETLQIIRRECLTNKPRYAGTSESHKKCTALELLEQEHTQGFIIT
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/protein_id="AAH00667.1"
/db_xref="GI:12653763"
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/clone="MGC:2023 IMAGE:3350026"
                                  FCSALDDILGGGVPLMKTTEICGAPGVGKTQL*
                                                                                                                                                                                                                /codon_start=1
                                                                                                                                                                                                                                                                         /note="Vector: pOTB7"
                                                                                                                                                                                                                                                                                                         /tissue_type="Eye, retinoblastoma"
/clone_lib="NIH_MGC_16"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                   .443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ctaggtgacagctggtcccactcatgcacgaaccggttgattctgcactggaatgggaac 1071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (19-OCT-2000) Siaud N., Reparation/Recombinaison de l'ADN Chez Arabidopsis, Institut de Biotechnologie des Plantes, Batiment 630, Universite Paris XI 91405 Orsay Cedex, FRANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATH296174 2340 bp DNA
Arabidopsis thaliana rad51C o
AJ296174
AJ296174.1 GT:11064474
RAD51C gene; Rad51C protein.
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1 (bases 1 to 2340)
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Similarity 51.9%;
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/number=1
join(166. .340,553. .639,742. .864,947. .980,1063. .1133,
1212. .1438,1549. .1680,1766. .1832,1929. .2104)
/gene="rad51C"
                                                                                                                                                              166.
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                                                                                                                                                                                                                                                /map="locus AAB82635"
/clone_lib="clones Tl
                                                                                                                                                                                                                                                                                                             /db_xref="taxon:3702"
/chromosome="II"
                                                                                                                                                                                                                                                                                                                                                                  /organism="Arabidopsis thaliana"
/cultivar="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                           /gene="rad51C"
                                                                                                                                                                                 /gene="rad51C"
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                      complete sequence. Sequence AC002387 AE002093 AC002387.2 GI:6598365
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1929. .2104
/gene="rad51C"
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a 436 c
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/Product="Rad51C protein"
/Product="Rad51C protein"
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/db_xref="G1:11064475"
/db_xref="G1:11064475"
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LSSIASVSSSDLARDANITEEEAFEILKLANQSCCNGSRSLINGAKNAWDMLHEEESL
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IYIDTEGSFMVERALGJAEAVYEDMEBYTGYMKHFTQANQVQMKPEDILENIFYFRVC
SYTEQIALVNHLEKFISENKDVKVVIVDSITFHFRQDYDDLAQRTRVLSEMALKFMKL
AKKFSLAVVLLMQVTTKFSEGSFOLALALGDSWSHSCTNRVILYWNGDERYAYIDKSP
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742. .864
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/gene="rad51C"
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947. .980
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="rad51C"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prediction programs including GRAIL

(ftp://arthur.epm.ornl.gov/pub/xgrail), Genefinder (Phil Green,
University of Washington), Genscan (Chris Burge,
http://gnomic.stanford.edu/GENSCANW.html), and NetPlantGene
(http://gnomic.stanford.edu/GENSCANW.html), and NetPlantGene
(http://www.cbs.dtu.dk/services/NetGene2/), searches of the
complete sequence against a peptide database and plant EST
databases at TIGR, and manual curations based on those analyses.
Annotated genes are named to indicate the level of evidence for
their annotation. Genes with similarity to other proteins are named
after the database hits. Genes without significant peptide
similarity but with EST similarity are named as 'unknown' proteins.
Genes without protein or EST similarity, that are predicted by two
or more gene prediction programs over most of their length are
annotated as 'hypothetical' proteins. Genes encoding tRNAs are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l (bases 1 to 122871)
Lin, X., Kaul, S., Rounsley, S.D., Shea, T.P., Benito, M.-I., Town, C.D., Fuji, C.Y., Mason, T.M., Bowman, C.L., Barnstead, M.E., Feldblyum, T.V., Buell, C.R., Ketchum, K.A., Lee, J.J., Ronning, C.M., Koo, H., Moffat, K.S., Cronin, L.A., Shen, M., Vanaken, S.E., Umayam, L., Tallon, L.J., Gill, J.E., Adams, M.D., Carrera, A.J., Creasy, T.H., Goodman, H.M., Somerville, C.R., Copenhaver, G.P., Preuss, D., Garenan, W.C., White, O., Elsen, J.A., Salzberg, S.L., Fraser, C.M. and Weiterman, W.C., White, O., Elsen, J.A., Salzberg, S.L., Fraser, C.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Medical Center Dr., Rockville, MD 20850, USA
On Dec 17, 1999 this sequence version replaced gi:2583106.
The sequence and annotation of chromosome 2 were merged from those of the individual clones on this chromosome after removing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           like to thank the TIGR Bioinformatics Department, especially Lixin Zhou, Hanif Khalak, Michael E. Heaney, Lily Fu, Feng Liang, Jeremy Peterson, Michael Holmes, and Delwood Richardson for software and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F13D4, and Scott Jackson, Jiming Jiang, Klaus Meyer, Eric Richards and Satoshi Tabata for helpful assistance. In addition, we would
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genes were identified by a combination of three methods: Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               overlaps. For detailed information, please see the TIGR web site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (09-MAR-2000) The Institute for Genomic Research,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Venter,J.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                Address all correspondence to:
                                                                                                                                                                                                                                                                                                                                                                                                                     This work was supported by the National Science Foundation, Department of Energy and the US Department of Agriculture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F6P23, F5J6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      We thank the CSHL/WashU/ABI consortium for sequencing BAC clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://ftp.genome.washington.edu/RM/RepeatMasker.html). Genes are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats were identified by repeatmasker (Arian Smit,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      predicted by tRNAscan-SE (Sean Eddy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (http://www.tigr.org/tdb/at/at.html)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           support.
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complement(519. .627)
                                                                complement(<1. .2952)
                                                                                                                                                                                          /organism="Arabidopsis thaliana"
/cultivar="Columbia"
                                    /note="Sequence from clone T14P1"
                                                                                                             /chromosome="II"
                                                                                                                                                      /db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                location,
                                                                                                                                                                                                                                                                           .12287
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                                                                                                                                                                                                                                                                                                            /Qualifiers
                                                                                                                                                                                                                                                                                                                                                    at@tigr.org
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16252. .16341,16810. .17006,17451. .17647))
/gene="At2945200"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(6393. .6470,6586. .6663,7082. .71 7248. .7296,7872. .8004,8099. .8260,8382. .8495))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /rpt_family="POLY_A"
complement(join(<6393. .6470,67248. .7296,7872. .8004,8099.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="maskalavtallitunlleftevtstkcppttpkppktpkspkk
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anvlginlnvpidltllnycgkkvphgeqcs"
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DILHEYTQEFRRIKGNINSLREHAELLSSVRDDISEYKASGSMSPGVQVLRERASIHG
                                                                                                                                                                                complement(join(15632. .15729,15821. 16252. .16341,16810. .17006,17451. .1 /gene="At12945200"
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/gene="At2g45200"
                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="(GA)n"
12613. .12646
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slfktvtvrcgcctnllsvnmrsyvlpasnqlqlqlgphsyfnpqdileelrdapsnm
nmmmnqhptmndipsfmdlhqqheipkappvnrppekrqrvpsaynrftkeeigrik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(<6393. .>8495)
/gene="At2g45190"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (2953.
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3250. .3641)
/gene="At2g45170"
SISHIDDVIGQAQATRAVLGSQRSLFSDVQGKVKNLGDKFPVIRGLLGSIKRKRSRDT
                                                                                     /product="putative cis-Golgi SNARE protein"
/protein_id="AAB82642.1"
/db_xref="GI:2583133"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAAANVGVTPY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGNPD I SHREAF SAAAKNWAHF PH I HFGL V PDNQ PVKKT NMPQQEGEDNMVMKEGF Y A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="putative proline-rich protein"
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/gene="At2g45180"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EDGFLYITYSGENTFGASSI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIDKKKYLVPSDLTVGQFVYVIRKRIKLSAEKAIFIFVDNVLPPTGELMSSVYEDKKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="putative microtubule-associated protein"
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                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="(CATA)n"
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/db_xref="GI:2583135"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="unknown protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="F4L23.30"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="F4L23.31"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Sequence from clone F4L23"
                                                                                                                                                                                                                                                                 /note="F4L23.29"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="At2g45180"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'gene="At2g45180"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rpt_family="(TAAAA)n"
                                                                                                                                                                      /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .>122871)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .6470,6586. .6663,7082. .7157,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .8260,8382. .>8495))
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.17583))
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Best
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                                                                                                                                                                                                                                                                                                  49147 AGAGGACATGGAAGAATACACAGGATACATGCATAAACATTTTCAAGCAAATCAAGTACA 49206
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                                                                                                                                                                                                                                                        705
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hes 174;
                                                                                                                            AATAATTTTGAAGTTCCATCCCGTTGATTTGCTGCTACAAGTGTATATTGTGACA 49381
                                       agttattattgatagtgttactttccactttcgacaagattttgaagatctggca 879
                                                                                               GCAAATCGCATTGGTCAATCATCTTGAAAAGTTCATCTCTGAAAACAAAGATGTAGGTAT
                                                                                                                                                                                                AATGAAACCAGAAGATATCTTAGAGAACATATTCTACTTCCGTGTCTGCAGTTACACCGA 49266
                                                                                                                                                                                                                           attacagcctgagcgtttcctggcggatatctattacttccggatatgcagttacaccga 764
                                                                                                                                                                                                                                                                                                                                                 tagggacatactggagcactttccgcacagccatgagaagtcctcttctgtccaaaaaca 704
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="putative pectinesterase"
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IKEALDAASGSGRFVIYVKQGYYSENLEIRKKNVMLRGDGIGKTIITGSKSVGGGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family="POLY complement(29132.
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28701. .28741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FNSATVAAVGDGFIARGITFRNTAGASNEQAVALRSGSDLSVFYQCSFEAYQDTLYVH
SNRQFYRDCDVYGTVDFIFGNAAVLQNCNIFARRPRSKTNTITAQGRSDPNQNTGII
IHNSRVTAASDLRPVLGSTKTYLGRPWRQYSRTVFMKTSLDSLIDPRGWLEWDGNFAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(join(22224. .22909,23488. .24334))
/gene="At2g45220"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(<22224. .>24334)
/gene="At2g45220"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(<22224. .22909,23488. .>24334))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="putative auxin-induced protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="At2g45210"
19741. .>20315
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19741. .>20315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="POLY_A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="At2g45220"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      family="POLY_A"
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Pred. No. 7.5e-14;
0; Mismatches 121
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REFERENCE

1 (bases 1 to 10980) Klenk, H.P., Clayton, R.A.,

Archaeoglobus.

Archaea; Euryarchaeota;

Archaeoglobales; Archaeoglobaceae;

Ketchum, K.A., Doo Richardson, D.L.,

Dodson, R.J.,

ton,R.A., Tomb,J., White,O., Nelson,K.E.,
dson,R.J., Gwinn,M., Hickey,E.K., Peterson,J.D.,
Kerlavage,A.R., Graham,D.E., Kyrpides,N.C.,

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RESULT 12
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           SOURCE
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                                                                                                                                                                                                                                                                                                                Query Match
Rest Local Similarity b1...
140; Conservative
 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence split into 28 fragments
                                                                                                                                  33116
                                                                                                                                                                                                                              32996 TGGCGGCGTCACCGAGATCAGTGGGCCCCCTGGCGTTGGCAAGACACAGCTGTTGATGCA 33055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LMFLCHR32_06
LMFLCHR32_07
LMFLCHR32_08
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LMFLCHR32_25
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LMFLCHR32_27
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LMFLCHR32_22
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LMFLCHR32_15
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LMFLCHR32_10
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LMFLCHR32_05
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LMFLCHR32_12
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                                                                                                                                              585 tatagatacagagggcagtttcatggttgaacgtgtctaccagattgc
                                                                                                                                                                                                         525
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                                                                                                                                                                                                                                                                                          CGTTGATACGGAGGGCAGCTTTGTGGCTGAGCGCTTAGAGCAAATGGC 33163
                                                                                                                                                                                 GCTAGCAGTTAGCTGTGCCATGCCAGTAGAGTTCGGAGGGATGGGTGGCGCGTGCCTTTT 33115
                                                                                                                                                                                                                                            caaagaagttactgagatcggtggcgtcccaggggttggtaaaactcaactggggattca 524
                                                                                                                                                                                                                                                                              GACCCACGTGACAACCTTCTCTGGGGAGCTCGACGGCGTACTTGGAGGTGGCGTTCCCGT 32995
Archaeoglobus fulgidus. Archaeoglobus fulgidus
                                   AE001035 AE000782
AE001035.1 GI:2689358
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                                                                      10980 bp
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500001
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300001
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                                                                                                                                                                                                                                                                                                                                      Score 87.2; DB Pred. No. 2e-10;
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                                                                       DNA
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                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                      base 1700001 (AL499622 Leishmania major
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                                                           72 of 172
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                                                                                                                                                                                                                                                                                                                            88;
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                                                        of the complete genome.
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                                                                                                                                                                                                                                                                                                                                                   Length 110000;
                                                                       15-DEC-1997
                                                                                                                                                                                                                                                                                                                            0;
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (15-DEC-1997) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA. In order to show the genes in ascending order on the genome, the origin of this version has been moved by TIGR to position 2093570 of the original version and the opposite strand is shown from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fleischmann, R.D., Quackenbush, J., Lee, N.H., Sutton, G.G., Gill, S., Kirkness, E.F., Dougherty, B.A., McKenney, K., Adams, M.D., Loftus, B., Peterson, S., Reich, C.I., McNeil, L.K., Badger, J.H., Glodek, A., Zhou, L., Overbeek, R., Gocayne, J.D., Weidman, J.F., McDonald, L., Utterback, T., Cotton, M.D., Spriggs, T., Artlach, P., Kaine, B.P., Sykes, S.M., Sadow, P.W., D'Andrea, K.P., Bowman, C., Fujli, C., Garland, S.A., Mason, T.M., Olsen, G.J., Fraser, C.M., Smith, H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus Nature 390 (6658), 364-370 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Woese, C.R. and Venter, J.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /Gene="AR0993"
/gene="AR0993"
complement(971. .1984)
/gene="AR0993"
/gene="AR0993"
/note="similar to GB:L77117 SP:Q49593 PID:1378034
/note="similar to GB:L77117 SP:Q49593 PID:1378034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PID:1591553 percent identity: ! sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="hypothetical protein; identified by GeneMark;
putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:2234"
159. .962
                                                                                                                                                                                                    SELANYGGITEGNAVKIIQAARKLANIGGFESGDKVLERRRSVKKITTGSKDLDELLG
GGVETQAITEFFGEFGSGKTQICHQLAVNVQLPEDEGGLEGSVIIIDTENTFRPERII
                                                                                                                                                                                                                                                                                                  /product="DNA.repair protein RAD51 (radA)"
/protein_id="AAB90248.1"
/db_xref="GI:2649602"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(971. .1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EVREAVKTAVQHTKECVKDLREIIQLINQYGDAEDSEELMQVVEEVVEE"
                                                                                                                                     QMAEAKGLDGNEVLKNIYVAQAYNSNHQMLLVDNAKELAEKLKKEGRPVRLIIVDSLM
SHFRÀEYVGRGTLADRQQKLNRHLHDLMKFGELYNAAIVVTNQVMARPDVLFGDPTKP
                                                                                                                                                                                                                                                                                                                                                                                                        /transl_table=11
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/gene="AF0994"
                                                                                                     VGGHIVAHTATFRIYLKKGKDDLRIARLIDSPHLPEGEAIFRVTERGIEDAEEKDKKK
                                                                                                                                                                                                                                                                          translation="MSEESNEETKIIELEDIPGVGPETARKLREAGYSTIEAVAVASP/
                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'gene="AF0992"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Archaeoglobus fulgidus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1997 this sequence version replaced gi:2649594.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF0992"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /Qualifiers
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/Translation="MFKEANRLTYIGYRLFAEDIMKKESKYFELERSLKKAMISMPPE
/YIATARMESLLFGIIGAVELTYKTIGYRLFAEDIMKKESKYFELERSLKKAMISMPPE
/YIATARMESLLFGIIGAVELTYKTYVGVPPFFINIRLEDIATYWLFYRFFVY
AGILAJGITLALYYLGAVLIFATYPSTVISDRKSKINRTLPHAIIFMYSLSKGGMSLVO
ILKALADNHEVYGEVSKEASRILMEVEGLGKDLRTALAEAVDTTPSDNFKEFLHGLIT
ILDSGGJITRYEEERABEYFEBARODOKSFLEFLGLMAETYITAFVAGFLFLIIIQTV
MSVMGOTNEVAMFSIIYFVIPTGSFWFAMLIKLTPGEBGSAPRLRERYIVRRSSEL
DSEEKKKLEKKVSRYKLMKKLKNPFRLIVENPLYTFAFSIPAALVILIYGLVNPYIF
GNDLKNNFFSYDDYIFISLKELAKIKADLDWGISLSCDALVRFARRLKIFEISRFWTLL
MPIYRAITMLAKTDTSSPLTKELAKIKADLDWGISLSCDALVRFARRLKIFEISRFWTLL
NEALKSTGNVTEVLMISAKDATSAELLRRERMINMFMYVIIYYIAFFVFIGITYIISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="similar to GB:L77117 SP:Q58310 PID:1591575 percent identity: 41.71; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MSSHDEGHVERVIKLARYIAEREGARLDVVLKAAELHDIARGYP NHARKSAEIABELLKOHDAEFYEAVCHAIEAHSFSGKMKPKTLEAKILSDADKLDAIG AIGVARAFLYSGEKGKSIEETLKHFEEKLLKLRDLLYTETARKIAEERHRFLEIFYRQ IKKELDEFEAEQDAEDYVGNGGHYK"

COMPLEMENT (2532. .4487)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(4489. .6198)
/gene="AF0996"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(4489.
/gene="AF0996"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AISLFIPRRSKIVTIEDTRELMLPHENWIPAVTRDAFHGEKGAVDMYDLLRAALRORP
EYIIYGEVRGKEALTLEQAMATGHTTYSTLHADSISGAHHRLENPPIGVERPMLEALD
IISLQAQTYYGDRRVERMEIAEIVGLDAHTKHLRTSTVFGWDSVKDEHAMVGTSKAL
EEIRRQRGWSVRELNEELERRRRVLEFMLEHNVRDFKRVSNIIHTYQTKPDKIMEAIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MPKINFRQLKFRGKEQEESEEEAEQLADYEKEALEAIESVKQK
EEILKVKTEKKKIIGLÞKKESYSVEHIGSLKNKLENKFEDGKVAKEVVLKETFDDL
NEEBGEYRKQVEPRLDFSTEVYGHIGSLKNKLENKFEDGKVAKEVVLKETFDDL
ISEVGFDLEDRSYYKIWYYIMRDFLYYDKITPLMLDKMLEDISCNGVRKYMYVFHRNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="type II secretion system protein (gspE-3)"
/protein_id="AAB90245.1"
/db_xref="GI:2649599"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAGAKHSLIMLTIAYIVFSVLFGFKLI"
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/trans1_table=11
/product="conserved hypothetical protein"
/protein_id="AAB90246.1"
/db_xref="GI:2649600"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="similar to GB:L77117 PID:1591923 percent identity:
26.90; identified by sequence similarity; putative"
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/protein_id="AAB90247.1"
/db_xref="GI:2649601"
                                                                                                                                                                                                                                                                 /note="similar to GB:L77117 PID:1592173 percent identity: 44.50; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                   complement(6259. .7509)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(6259. .7509)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TNLRTNVIFDDPDELDSFVVNLAQKCGKHISIAEPMVDATMPDGSRIQMTLGREVTDH
GSTFTIRKFREEPVTPIDLIAWKTFSSEQMAYLWLCIENKKSLIFAGGTASGKTTSMN
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                                                                                                                                                                                           /transl_table=11
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DEFINITION
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Best Local (
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                                                                                                                                                                                                                  1490 G 1490
                                                                                                                                                                                                                                                                                                                          1550 GATTATCATCGACACAGAGAACACATTCAGGCCTGAGAGGGATAATCCAGATGGCTGAGGC 1491
                                                                                                                                                                                                                                                                                                                                                                                                                                1730 GTCTGTTAAGAAAATAACTACTGGGAGCAAAGACCTCGACGAGTTGCTTGGTGGTGGAGT 1671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    459 tcactgcaaagaagttactgagatcggtggcgtcccaggggttggtaaaactcaactggg 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            399 gtcacagaaacacatcactactggttctggtgacctcaatgacatacttggtggcgggat 458
                                                                                                                                                                                                                                                                                                                                                                          579 agtttatatagatacagagggcagtttcatggttgaacgtgtctaccagattgctgaagg 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gattcaactagcaatcaatgtacaaatcccagtggaatgtggtggccttggtgggaaagc 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGAGACCCAAGCCATAACCGAGTTTTTTGGAGAGTTTTGGTAGTGGTAAGACTCAAATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139;
Methanobacterium thermoautotrophicum from bases 1243964 to 1257931 (section 107 of 148) of the complete genome. AE000901 AE000666
                                                                              AE000901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="conserved hypothetical protein"
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/db_xref="GI:2649597"
/translation="MNVLLSRKDTIRFLILSELMVNPECNORDIAKKIGLTPOAISEH
/translation="MNVLKSRKDTIRFLILSELMVNPECNORDIAKKIGKTVVAIAKGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="hypothetical protein; identified by putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="AF0998"
7581. .8357
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RYGKRPVEFLDSIGFLDSSTVLAHAVWLSEAEMKILAERGVSVAHCPTSNLKLSSGIA
KVSELLEMGVNVGIGTDGAASNNMLSVLSDARVGALLQNLRGRTLKPGHWLEMATEGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(9003. .9746)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="mkGalllvllILTISTTSAVEIYGKVYRWDTLDVLSGAVVEVRD
GSVQRMVAENGEYSFNVTPGNYTIIARSGEYYAIENVTVSSDMRFDLILFPSLEEVEE
IPDFPVVDQQEEFPYYIVAILVSGFVLAALFIVKIRSEKQPELLEQEVTPEEYDLPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(8350. .9006)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="AF0999"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(8350. .9006)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAHHGSGVIVACTESMLNDLLRSLIDEGLEFEIKEFVKAT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IAENDSVRYWFGDGYIFAERSAKGNGVÄLTSAEDGEDVLIKPTGSFEPPEKGEIIIVK
VPGVAEGGSRKVDLDSFRELVKSRPTSIVVAIGIEALVTCRKIRVEPIFFGAKEVCIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ILVNVEEEKVIEKAEETALELVGG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YRAYNLKGGRIEEGYLADIVVFSKTCRNAPMHDPAAMLYVENQALHAVVDGVLVMEDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="AF1000"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LAEYVELIKREGGRITQKELRKKLGYSEAKMSLIIADLERRGIVEKVKKGRGNIIFLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /transl_table=11
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/protein_id="AAB80250.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="AF0999"
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identity: 27.52; identified
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                                                                              13968 bp
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57.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102;
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by sequence similarity;
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TITLE
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Aldredge,T., Bashirzadeh,R., Blakely,D., Cook,R., Gilbert,K.,
Harrison,D., Hoang,L., Keagle,P., Lumm,W., Pothier,B., Qiu.D.,
Spadafora,R., Vicaire,R., Wang,Y., Wierzbowski,J., Gibson,R.,
Jiwani,N., Caruso,A., Bush,D., Reeve,J.N. et,al.
Complete genome sequence of Methanobacterium thermoautotrophicum
deltaH: functional analysis and comparative genomics
J. Bacteriol. 179 (22), 7135-7155 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Methanothermobacter thermautotrophicus Methanothermobacter thermautotrophicus Archaea; Euryarchaeota; Methanobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Therapuetics Corporation, 100 02154-8448, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (10-AUG-1997) Genomics and Technology Development, Genome Therapuetics Corporation, 100 Beaver Street, Waltham, MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smith, D.R.
Direct Submission
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/db_xref="GI:2622489"
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GIADTLYTNAVAQAGKGGVPVYCVPVDLEEGDVETVLPSKLELELCRGCEPCLAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Function Code:9.10 - Metabolism of Cofactors and Vitamins, Porphyrin and chlorophyll metabolism; similar to, sp:LN:CPCE_FREDI AC:P07126:P05520, p()=1.7E-09, pid=55%"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Function Code:14.01 - Unknown, Conserved protein; similar to, pir:LN:G64486 AC:G64486, p()=7E-10, pid=29%"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(502. .900)
/gene="MTH1378"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(502. .900)
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                                                                                                                                                                                                                                                                                              complement(1027. .1737)
/gene="MTH1379"
                                                                                                                                                                                                                                                                                                                                                    complement(1027. .1737)
/gene="MTH1379"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="conserved protein"
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/db_xref="GI:2622487"
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/db_xref="taxon:145262"
                                                                                                                                                                                                                     pid=48%"
                                                                                                                                                                                                                                                                                                                                                                                                         EALDDEDYHVREAAALALATFDDRMAVEPLREHLSDDKPGVRYACALALGILGDEDSI
PDLEELLDDESPMVRRVAEVAISEIRKRAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPVGRGRYGSGIHMFFMLVPLDVLFVDGDMRVVDSVTLRPWQIYNPRKPARYVIELRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="MTH1377"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MMKREVINKTRGTSLGAVRFARTFMSRFRGLMLRRDVETGLVLE/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="MTH"
                                                                                                                                                                   /transl_table=11
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                                                                                                                                                                                         'codon_start=1
                                                                                                                                                                                                                                                                           note="Function Code:14.01 -
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                                                                                                                                                                                                                                            tion Code:14.01 - Unknown, Conserved protein; sp:LN:Y208_METJA AC:Q57661, p()=1.2E-51,
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IEMPNIFDEGIGMTKAVYIPFDQAVCATIOKDYCIEGMLODEDIGEGGAVKHDQEPE
EIELEWGTILVATGUDAYDPTEKLEVGYGRFFUNVITGLELERWINASGFDGKVIKSP
DGEKPKRVAFIHCVGSRDEQIGKPYCSRVCCMYIMKNAQLIKDKMPDTEVTLYYMDIR
AFGKGFEEFYKRSQEKYGIKFIRGRAEILENPDLTLTVRSEDTLAGKVTEYDYDMVV
LGVGLVPPEGSEKLRQTGLSKSADGETMEAHFKLRPVDTJTDGVYLAGVAQGFKDIP
DAVAQASGAAARAAIPMVKGEVFIEPIVAVTDSDVCGGCEVCIELCPFGAISIEEGHA
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/gene="MTH1881"
complement(3192. .5201)
/gene="MTH1381"
/gene="MTH1381"
/gene="MTH1381"
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/note="Function Code:10.08 - Metabolism of Macromolecules,
Protein translation and modification; similar to,
pir:LN:S48720 AC:S48720, p()=0, pid=88*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="G1:2622492"
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/gene="MTH1382"
/note="function Code:14.01 - Unknown, Conserved protein;
similar to, pir:LN:F64428 AC:F64428, p()=3.7E-20, pid=24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product-"heterodisulfide reductase, subunit A "
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VDIAGNAEMPRIGVTMAEMPRIGVTMAEKTYMVEKRPSISGRMGQLDKTTPTLDCSMCILL
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                                                                                pid=51%"
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                                                                                                                                                                                                                                                                                          complement (6276.
                                                                                                                                                                                                                                                                                                                                                                     VDLVSSCIFMSTILSLVSLPLWSVVL" complement(6276. .7211)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          RAVEFPPLWAFLLGVIFNLWGLPTGIAGTILGYLSGAAVPLIMISLGLTLNFRFLRHS
VADATLVSGLRLLISPLWAAGISYVLAFRGLNFSVTVLEASMPSAMLAAVLAIENDLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(5353. .6261)
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/transl_table=11
                                                                                                                                                                                                                                                                                                                           /gene="MTH1383"
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SKRLEANNIILNKNLLPWDDVNRSDDPSGIRIGTQEITRRGMKESEMSEVAEYIKRVV
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LREGADMLVGSTHKTFPGPQGGIILCREELAADIDEAVFPGLVSNHHLHHVAGLGIAT
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NLACFFATAEVGDPIMAMEVPYGGHISHARVSAAGVRGFQIYTHPFDFENMNIDADAM
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RVFAKPGEILENMAHSHI"
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/transl_table=11
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652 atactggag 660
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                                                                                                                                                                                                                                                                                                                                                             atcaatgtacaaatcccagtggaatgtggtggccttggtgggaaagcagtttatatagat 591
                                                                                                                              ACAGAGAACACATTCCGTCCTGAGAGGATTGAGCAGATAGCAAATGCCTTTGAACTTGAC
                                                                                                                                                                                             acagagggcagtttcatggttgaacgtgtctaccagattgctgaagggtgtattagggac 651
                                                                                                                                                                                                                                                                                          GTCACGGTTCAGCTGCCAGAGGAGGAGGAGGAGGACTGGATGCTGAGGCTGTTTTCATAGAC
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/gene="MTH1385"
complement(7775. .9643)
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56.2%;
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412 atcactactggttctggtgacctcaatgacatacttggtggcgggattcactgcaaagaa 471
ATCACAACGGGGAGCAAGGCCCTCGATGAACTGATAGGTGGCGGAATCGAGACACAGGCA 6918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="replication factor A related protein"
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TVEVLDPEDYPEEFPEYREEITPIGDLVEDDEVNVIARITGVSRVRTFERDGREGRFIS
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PGEYDVPEFREELVKIGDLHEMRNUTVMGLUTKVNDEVEFERNDGTTGSVKSIEIADD
TGSARVTLHDEDTRIKIKGDLHEMRNUTVMGLUTKVNDEVEFERNDGTTGSVKSIEIADD
TGSARVTLHDEDTRIKIKGENIRISGDEOEDVOGRIFSSYSTENTUTLNPSDGA
LLKVLEEYROMRPMKISEILEMEDBGGEVDVVGRIFSLSDDREFEREDGTGIVRSME
LADDETGKIRISLAMDEKAEKPMNIGDAVRIENARIRLGLYSVELSAGRTTRIVNFLPED
MEDLPSFEELEEMLYQTKKIADLEEDDRNIRIIARVVDLFEPREFQRGDGTPGLVRTA
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SRNVLIEGELIEMSGRRILSIKCPSCNERLDLSDENICNFCGELVDEPRYLLMIPGRI
MDDTGEVMITFFGREAESILEMTTDEVVNIINQSADESALEERVEDLNGVTVRVIGNA
DMDVYSEELRFIPRKVVKKEL"
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EVLNKIHIARAFNSSHQILMAEKVNELIQEGKNIRLVIVDSLTAHFRAEYVGREALAT
RQQKLNQHLHTLQNIANTYNAAVFVTNQVQARPDAFFGSPTKAIGGHVLGHAATYRIW
                                                                                                                                                                                                                                                                                                                                                                          EFADDTGSIRASLWDDAAEKPLSIGDPVKIENPRVVFRDDMGGGRLETQHRKQFKD"
9947. .11206
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egvaekvieaarraekidfetafdvmerrkdvgrittgskaldeligggietqaitev
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/protein_id="AAB85860.1"
/db_xref="GI:2622493"
                                                                                                                                                                                                                                                                               Length 13968;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                            538 AAAGAAGCGAGAGACGCATTAGATATAAGATTTAAGACGGCCCTGGAAGTCAAAAAGGAG 597
                                                                                                                                                                                                                                                                                                                                                                                                     334 aatggaccacaacagaagtacgtttcaggagcccagaatgcctgggatatgttctctgat 393
                                                                                                                                                                                                                      454 gggattcactgcaaagaagttactgagatcggtggcgtcccaggggttggtaaaactcaa 513
                                                                                                                                                                                                                                                                      598 AGAATGAACGTTAAGAAGATATCTACTGGTAGTCAAGCATTAGATGGTCTTTTAGCTGGA 657
                                                                                                                                                                                                                                                                                                               394 gagctgtcacagaaacacatcactactggttctggtgacctcaatgacatacttggtggc 453
                                                                                                                     514 ctggggattcaactagcaatcaatgtacaaatcccagtggaatgtggtggccttggtggg 573
                          574 aaagcagtttatatagatacagagggcagtttcatggttgaacgtgtctaccagattgct 633
778 AAGGCAGTTTACATTGATACAGAAGGTACTTTCAGATGGGAAAGAATTGAAAATATGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                               GGTATAGAAACTAGAACTATGACGGAATTCTTCGGTGAGTTTGGGTCTGGTAAAACACAG 717
                                                                                      CTATGTCATCAGTTAAGTGTTAATGTACAACTACCACCAGAGAAAGGTGGCTTATCTGGT 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sulfolobus solfataricus radA gene, complete cds.
U45310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (11-JAN-1996) Steven J. Sandler, Molecular and Cell Biology, University of California, 401 Barker Hall #3202, Ber CA 94720-3202, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sandler, S.J., Satin, L.H., Samra, H.S. and Clark, A.J. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      products similar to Rad51 and Dmc1 proteins of the yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sandler, S.J., Satin, L.H., Samra, H.S. and Clark, A.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sulfolobus solfataricus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EYPGREILAVRQOKLNKHLHOLTRLAETYDIAVIITNOVMARPDMEYGDETVAVGGHT
LYHVPGIRIQLKKSRGNRRIARVVDAPHLPEGEVVFALTEEGIRDAEE"
223 c 354 g 507 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Sulfolobus solfataricus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="RadA"
/protein_id="AAC44123.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transl_table=11/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="RecA-Rad51 homolog"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.9%; Score 72; DB 3; Length 1699 52.3%; Pred. No. 7.7e-07; ative 0; Mismatches 145; Indels
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AP000058 BA000002
AP000058.1 GI:5103388
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Kawarabayasi, Y. is officially affiliated with the National
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tanaka, T., Hino, Y., Kawarabayasi, Y. and Kikuchi, H. Direct Submission
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99310339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (14-DEC-1998) to the DDBJ/EMBL/GenBank databases. Yutaka
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    information are available at W.W.W. site of Biotechnology Center, URL: http://www.mild.nite.go.jp/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and stop codon are defined as CDS Homology analysis is performed by Smith-Waterman algorithm against GenBank and GenPept release 109; EMBL release 56.0; SwissProt release 36.0; PIR-Protein release 57.0; and OWL release 31.0. E-mail address for comments and questions: genomeAPE@nite.go.jp Restriction map, ORF organization, sequence alignment and more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The other authors are at the National Institute of Technology and The Other authors are at the National Institute of Technology and The Other 2-49-10 Nishihara, Shibuya, Tokyo 151-0066, Japan.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Evaluation, 2-49-10 Nishihara, Shibuya, Tokyo 151-0066, Japan.
All the sequence with length 100 codons or more between ATG or GTG
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Nomura, N. and Sako, Y. are at Kyoto University, Sakyo-ku, Kyoto
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                                                                                                                                                                                                                                                                                    complement(213. .938)
/gene="APE0001"
                                                                                                                                                                                                                                                                                                                                  complement(213. .938)
/gene="APE0001"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pernix
                                                                                                                          /translation="MYDILSSLLLSLPFGVIGFLLVLSPGSIWTPVKESIGYVYVSRR
VTVKASKLLGSLTLLASLISFYVGAAYGITIQASTLALLLALITVVTVEYSMRLAEIE
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/db_xref="GI:5103389"
                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Aeropyrum pernix"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .202000
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                complement(938. .1276)
/gene="APE0002"
                                                                                                       SLNQPVLEGFEPVGSIKLKYLTIILLVYLISIVFSIEGSLKLYSIGAYGTLASHLSIE
                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:56636"
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                                                                                                                                                                                                                                           /transl_table=11
                                                                                                                                                                                                                                                                   /codon_start=1
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3896. .5440
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2261. .2836
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APLASYVMSLPIAKALGVSIGPCGYFKEVSNTTLLITTVIILILLGLIAGVTNNALVA
GEELGWRGYLFTILDKKVNNDLGKVIIIGLIMSVWHAPLIYAGYNYNVSMLGDCGSYS
GGWPAAIVVFTLYTIAFTSILLPLRRHENSIITPAIAHGTVNGIGGVFAALTIGNRLVA
                                                                                                                                                                                                                                                                                                                                                    /transl_table=11
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/db_xref="GI:5103393"
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1618. .2091
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/db_xref="01:5103392"
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                                                                                                                                                                                                                                                                                                                                                                                                  /gene="APE0006"
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/gene="APE0004"
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'anchoring' hexapeptide"
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1225. .1527
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                                                              89207 CAAGACCGCTTACGACCTGAAGATCGAGAGCATGAACATTAAAAAGATTACGACGGGGAG 89266
                                                                                                                                                                                                                                                                            CDS
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426 tggtgacctcaatgacatacttggtggcgggattcactgcaaagaagttactgagatcgg 485
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                                                                                                   366 ccagaatgcctgggatatgttctctgatgagctgtcacagaaacacatcactactggttc 425
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                                                                                                                                                                                    Local Similarity
                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                       /gene="APE0011"
8251. .8889
                                                                                                                                                                                                                                                /gene="APE0011"
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                                                                                                                                                                                                                                                                                                                                                                                         VYQMASMNPGELAILAVLIAGSMAAEALYRRIKGRRLPQVIDPSLKVRESLISGWRNL
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RVEPPILVFETLTPEGEVLWAREIAVDIEQGKLLGFRENSLYFTDGRYVYKKGPDRAA
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Score 71.4; DB 2; Length 202000;
Pred. No. 1.4e-06;
0; Mismatches 126; Indels 0;
    0; Gaps
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Post-processing: Minimum Match 0%
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000 Comp
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900.010 million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Database :

SwissProt\_39:\*

## SUMMARIES

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140 ADIYYFRICSYTEQIAVINYMEKFLREHKDVRIVIIDSVTFHFRQDFEDLALRTRVLSGL 199

Query Match 37.7%; Score 576.5; DB 1; Length 376; Best Local Similarity 43.9%; Pred. No. 2.2e-42; Matches 125; Conservative 47; Mismatches 98; Indels 15;

Gaps

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## ALIGNMENTS

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125 132 76 AA; 42189	oinding; Nuclear	ITE; PS50	MIN ROOTIA	33030604 1.	nd an email to license@isb-sib.ch)	ee }		by non-profit institutions as long as its content is in no	Bioinformatics Institute. There a	Inls SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -		RECA PROTEIN.	UKARYOTIC RECA	HIGHEST EXPRESSION IN TESTIS, HEART MUSCLE, SPLEEN AND		-!- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).	Nucleic Acids Res. 26:1179-1184(1998).		"Isolation and characterization of RAD51C, a new human member of the		Dosanjh M.K., Collins D.W., Fan W., Lennon G.G., Albala J.S., Shen Z.,	MEDLINE-98136197; PubMed=9469824;	SEQUENCE FROM N.A.	[1]		Primates; Catarrhini; Hominidae;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens (Human).	RAD51L2 OR RAD51C.	DNA REPAIR PROTEIN RAD51 HOMOLOG 3.	Last annotation	(Rel.	(Rel.	043502;	R51C_HUMAN STANDARD; PRT; 376 AA.	RESULT 1

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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50162; RECA_2; 1. PROSITE; PS50163; RECA_3; 1.
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MEDLINE=96251095; PubMed=8668545;
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                                                                                                                                                                                                                GKTQLCHQLSVNVQLPPEKGGLSGKAVYIDTEGTFRWERIENMAKALGLDI------
                                                                                                                                                                                                                                                              GKTQLGIQLAINVQIPVECGGLGGKAVYIDTEGSFMVERVYQIAEGCIRDILEHFPHSHE 124
                                                                                                                                                                                                                                                                                                                        QKIIKEARDALDIRFKTALEVKKERMNVKKISTGSQALDGLLAGGIETRTMTEFFGEFGS 118
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FP (POTENTIAL).
B08CA699AA404A88 CRC64;
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RADA_ARCFU
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Matches
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restricted the companion of the companion of the control of the companion of
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15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA damage; DNA recombination; NP_BIND 115 122 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50162; RECA_2; 1. PROSITE; PS50163; RECA_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE001035; AAB90248.1; TIGR; AF0993; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
-i- FUNCTION: PROBABLY INVOLVED IN DNA REPAIR AND IN HOMOLOGOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98049343; PubMed=9389475;
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SIMILARITY: STRONG TO EUKARYOTIC RECA-LIKE PROTEIN; SOME, TO PROKARYOTIC RECA PROTEIN.
ERFLADIYYFRICSYTEQIAVIN----YMEKFLREHKDVRIVIIDSVTFHFRQDF---ED
                                                                                          NVQLPEDEGGLEGSVIIIDTENTFRPERIIQMAEA----
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                                                                                                                                             NVQIPVECGGLGGKAVYIDTEGSFMVERVYQIAEGCIRDILEHFPHSHEKSSSVQKQLQP 135
                                                                                                                                                                                                                                                                                                                            l Similarity
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Pred. No. 2.
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A Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
A Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
A Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
A McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
A Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.,
Complete genome sequence of Methanobacterium thermoautotrophicum
Complete genomics State Stat
                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                           Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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15-DEC-1998 (Rel.
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                                                                       FGSGKSQLSHELAVTVQLPEERGGLDAEAVFIDTENTFRPERIEQIANAF-----
                                                                                                                                                                                                                           GPQQKYVSGA-----QNAWDMFSDELSQKHITTGSGDLNDILGGGIHCKEVTEIGGV
                       SHEKSSSVQKQLQPERFLADIYYFRICSYTEQIAVINYMEKFLREHKDVRIVIIDSVTFH
                                                                                                                            PGVGKTQLGIQLAINVQIPVECGGLGGKAVYIDTEGSFMVERVYQIAEGCIRDILEHFPH 121
                                                                                                                                                                            GVAEKVIEAARRAEKIDFETAFDVMERRKDVGRITTGSKALDELIGGGIETQAITEVFGE 105
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                                                                                                                                                                                                                                                                                                                                                                                                               311 AA;
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Last annotation update)
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                                                                                                                                                                                                                                                                                46;
                                                                                                                                                                                                                                                                                                        Score 352.5; DB 1 Pred. No. 3.5e-23;
                                                                                                                                                                                                                                                                                                                                                                                                            3A0DF609A98785DB CRC64;
                                                                                                                                                                                                                                                                                Mismatches 111;
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                                                                                                                                                                                      AVILES E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M., Guzman E., Carpenter J., Chen E., Cherry J.M., Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C., Pettel F.X., Roberts D., Schl P., Schramm S., Shogren T., Smith V., Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.; Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: REQUIRED FOR MEIOTIC RECOMBINATION, SYNAPTONEMAL COMPLE FORMATION AND CELL CYCLE PROCRESSION.
                                                                                                                                                                                                                                                                                                                                                                                                                        Wei
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P25453;
                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                          STRAIN-S288C / AB972;
Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kobayashi T., Hotta Y., Tabata S.;
"Isolation and characterization of a yeast gene that is homologous with a melosis-specific CDNA from a plant.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=92257586; PubMed=1581960;
Bishop D.K., Park D., Xu L., Kleckner N.;
"DMCl: a meiosis-specific yeast homolog of E. or
recombination, synaptonemal complex formation,
                                                                                                                                                                             <del>'</del>
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
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01-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 progression."
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                                                                                                                               SIMILARITY:
PROKARYOTIC
                                                                                                                                                                           DEVELOPMENTAL
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                                                                                                                                                                                                                                                                                                                                                                                                                      Taylor
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1997 (Rel. 35, Last annotation update)
RECOMBINATION PROTEIN DMC1.
                                                                                                                                                                                                                                                                                                                                                                                                       J.T., Dietrich F.S., Hennessey K.M., Sehl P., aylor P., Nakahara K., Roberts D., Davis R.W.; (FEB-1993) to the EMBL/GenBank/DDBJ databases
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                                                                                                                              STRONG TO OTHER EUKARYOTIC RECA-LIKE PROTEIN; RECA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  237:225-232(1993).
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).

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EMBL outstation collaboration -L outstation -

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            015315; 060914;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation updat
DNA REPAIR PROTEIN RAD51 HOMOLOG 2 (R51H2).
RAD51L1 OR RAD51B OR REC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
EMBL;
EMBL;
PIR;
PIR;
PIR;
                     MEDLINE=98181067; pubMed=9512535;
Cartwright R., Dunn A.M., Simpson P.J., To
"Isolation of novel human and mouse genes
recombination-repair gene family.";
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (1ST FORM).

MEDILINE-97352813; PubMed-9207106;

Rice M.C., Smith S.T., Bullrich F., Havre P., Kmiec E.B.;

Rice M.C., Smith S.T., Bullrich F., Havre P., Kmiec E.B.;

"Isolation of human and mouse genes based on homology to REC2, recombinational repair gene from the fungus Ustilago maydis.";

Proc. Natl. Acad. Sci. U.S.A. 94:7417-7422(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50162; RECA_2; 1.
PROSITE; PS50163; RECA_3; 1.
Sporulation; Meiosis; Cell cycle; ATP-binding; Nuclear protein.
NP_BIND 121 128 ATP (POTENTIAL).
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (1ST FORM). MEDLINE=98110585; PubMed=9441753;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R51B_HUMAN
                                                                                                                            SEQUENCE FROM N.A. (2ND FORM)
                                                                                                                                                                                                     Thompson L.H., Lennon G.G.; "Identification of a novel human
                                                                                                                                                                                                                                                        Albala J.S., Thelen M.P.,
     Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
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D10865; BAA01637.1;

L; U18922; AAB64706.1;

S30857; S30857

S30857; S30857;

S30276; S30276;

A38214; A38214

A38214; A38214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ITTGSGDLNDILGGGIHCKEVTEIGGVPGVGKTQLGIQLAINVQIPVECGGLGGKAVYID 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VAVFLTNQVQS--DPGASALFASADGRKPIGGHVLAHASATRILLRKGRGDERVAKLQDS
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                                                                                                                                                                                46:476-479(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
     26:1653-1659(1998).
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ation update)
2 (R51H2).
                                                                                                                                                                                                        RAD51 homolog,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ·---YELDPESCLANVSYARALNSEHQM
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                                                                                                                                                                                                                                                        Fan W.,
                                                    Tambini C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
.2e-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93;
                                                                                                                                                                                                                                                          Christensen
                                                                            G
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                                                                                                                                                                                                             RAD51B.";
                                                    C.E., Thacker J.;
recA/RAD51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    254
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                                                                                                                                                                                                                                                                           DMC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                              Q61880;
Q1-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U92074; AAB63358.1;
EMBL; U84138; AAC39723.1;
EMBL; Y15571; CAA75680.1;
MIM; 602948; T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                     MEDLINE=96038268; PubMed=8581742; Sato S., Kobayashi T., Hotta Y., Tabat: "Characterization of a mouse recA-like
                                                                                                                                                                            METOTIC RECOMBINATION PROTEIN DMC1 OR DMC1H OR LIM15.
                                                                                                                                                                                                       01-NOV-1997
30-MAY-2000
                                                                                                                                                                                                                                                           MOUSE
DMC1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA-binding; ATP-binding; Nuclear protein; Alternative splicing.

NP_BIND 108 115 ATP (POTENTIAL)

VARSELIC 346 350 AA; 38257 MW; CEA992DDC394F3B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----
                          testis.";
                                                                               SEQUENCE FROM N.A. TISSUE=Testis;
                                                                                                           NCBI_TaxID=10090;
                                                                                                                                      Mammalia;
                                                                                                                                                  Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                                           236
                                                                                                                                                                                                                                                                                                                                                                                                                  198
                                                                                                                                                                                                                                                                                                                                                                                                                                            188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 135
                                                                                                                                                                                                                                                                                                                               297
                                                                                                                                                                                                                                                                                                                                                                                      237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: EXPRESSED IN A WIDE RANGE OF TISSUES.
SIMILARITY: STRONG TO OTHER EUKARYOTIC RECA-LIKE PROTEIN;
                                                                                                                                                               musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: NUCLEAR (PROBABLE). ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROKARYOTIC RECA PROTEIN.
                                                                                                                                                                                                                                                                                                                              GNTWSHSVNTRLILQYLDSERRQILIAKSPLAPFTSFVYTIKEEGL 342
                                                                                                                                                                                                                                                                                                                                                         GDSWSHSCTNRLILHWNGNERYAHL-DKSPSLPVASAPYAVTGKGI 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YYFRICSYTEQIAVINYMEKFLREHKDVRIVIIDSVTFHFRQDFE-----DLALRTRVLS 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDELSQKHITTGSGDLNDILGGGIHCKEVTEIGGVPGVGKTQLGIQLAINVQIPVECGGL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                          VLQRIESLEEEII--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGAVVYIDTESAFSAERLVEIAE-----SRFPRYFNTEEKLLLTSSKVHLYRELTCDE 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGKAVYIDTEGSFMVERVYQIAEGCIRDILEHFP---HSHEKSSSVQKQLQPERFL-ADI 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SADESPAFLSTTLSALDEALHGGVACGSLTEITGPPGCGKTQFCIMMSILATLPINMGGL 134
                                                                                                                                                                                                                                                                                                                                                                                      REASSLKYLAEEFSIPVILTNQITTHLSGALASQADLVSPADDLSLSEGTSGSSCVIAAL
                                                                                                                                                                                                                                                                                                                                                                                                            GLSLKLMKIAKTYNLAVVLLNQVTTKF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PS50162; RECA_2;
           2:147-150(1995).
                                                                                                                                     Eutheria;
                                                                                                                                                                                                       (Rel. 35,
(Rel. 35,
(Rel. 39,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                     Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21.1%; 32.2%;
                                                                                                                                                                                                       Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                             -----SKGIKLVILDSVASVVRKEFDAQLQGNLKERNKFLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 323;
Pred. No. 1.
                                                                                                                                   Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                         notation update)
DMC1/LIM15 HOMOLOG
                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                      Tabata
                                                                                                                                                                                                                                                              340
                                       gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100;
                                       specifically
                                                                                                                                      Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  ---TEGSFQLTLAL 235
                                                                                                                                                      Euteleostomi;
                                                                                                                                      Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         restrictions
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                                                                                                                                                                                                                                                                                                                                                                                        296
                                                                                                                                                                                                                                                                                                                                                                                                                                             236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
DMC1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                    DMC1_HUMAN STANDARD; PRT; 340 AA. 014565; Q99498; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-OCT-2000 (Rel. 40, Last annotation update) DMC1 OR DMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MSSF; FULL.
MSD; MGII105393; DMC1...
MCD; MGII105393; DMC1...
PROSITE; PS50162; RECA_2; 1.
PROSITE; PS50163; RECA_3; 1.
Meiosis; Cell cycle; ATP-binding; Nuclear protein.
                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; D58419; BAA09590.1; -. EMBL; D64107; BAA10969.1; -. HSSP; P03017; 2REB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Habu T., Taki T., West A., Nishimune Y., Morita T.;
"The mouse and human homologs of DMC1, the yeast melosis-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=129/SV; TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 HITTGSGDLNDILGGGIHCKEVTEIGGVPGVGKTQLGIQLAINVQIPVECGGLGGKAVYI 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KSPSLPVASAPYAVTGKGIRDA 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IAVINYM-EKFLREHKDVRIVIIDSVTFHFRQDFE---DLALRTRVLSGLSLKLMKIAKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DSPEMPENEATFAITAGGIGDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YNVAVFVTNQMT----ADPGATMTFQADPKKPIGGHILAHASTTRISLRKGRGELRIAKIY 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YNLAVVLLNQVTTKFTEGSFQLTLAL-----GDSWSHSCTNRLILH-WNGNERYAHLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MELLDYVAAKFHEEAGIFKLLIIDSIMALFRVDFSGRGELAERQQKLAQMLSRLQKISEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DTEGSFMVERVYQIAEGCIRDILEHFPHSHEKSSSVQKQLQPERFLADIYYFRICSYTEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HITTGSQEFDKLLGGGIESMAITEAFGEFRTGKTQLSHTLCVTAQLPGTGGYSGGKIIFI 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DTENTFRPDR------LRDIADRFNVDH------EAVLDNVLYARAYTSEHQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=8602360;
                                                                                                                          Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 314.5; D. Pred. No. 7.3e-
                                                                                                     Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                     Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Length 340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35;
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DMC1\_LILLO P37384; 01-OCT-1994 01-OCT-1994 01-NOV-1997

STANDARD;

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Best Local Similarity
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Meiosis; Cell cycle; ATP-binding; Nuclear protein.
NP_BIND 126 133 ATP (POTENTIAL).
CONFLICT 37 37 I -> N (IN REF. 2).
CONFLICT 183 183 P -> A (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D63882; BAA09932.1; -. EMBL; D64108; BAA10970.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sato S., Seki N., Hotta Y., Tabata S.; "Expression profiles of a human gene identified as a structural homologue of meiosis-specific recA-like genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50162; RECA_2; 1. PROSITE; PS50163; RECA_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Testis;
MEDLINE=96173646; PubMed=8602360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA Res. 2:183-185(1995).
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MEDLINE=96127532; PubMed=8590282;
                                                       307
                                                                                252
                                                                                                             250
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                                                                                                                                                                                              144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          602721;
                                                                                NGNERYAHLDKSPSLPVASAPYAVTGKGIRDA 283
                                                                                                          LSRLQKISEEYNVAVFVTNQMT----ADPGATMTFQADPKKPIGGHILAHASTTRISLRKG
                                                                                                                                     SLKLMKIAKTYNLAVVLLNQVTTKFTEGSFQLTLAL-----GDSWSHSCTNRLILH-W 251
                                                                                                                                                                                         YFRICSYTEQIAVINYM-EKFLREHKDVRIVIIDSVTFHFRQDFE---DLALRTRVLSGL 199
                                                                                                                                                                                                                                                                             EYSEKRKMVFHITTGSQEFDKLLGGGIESMAITEAFGEFRTGKTQLSHTLCVTAQLPGAG 149
                                                                                                                                                                                                                                                                                                       ELSQK-----HITTGSGDLNDILGGGIHCKEVTEIGGVPGVGKTQLGIQLAINVQIPVEC 83
                                                      RGELRIAKIYDSPEMPENEATFAITAGGIGDA
                                                                                                                                                                YARAYTSEHQMELLDYVAAKFHEEAGIFKLLIIDSIMALFRVDFSGRGELAERQQKLAQM
                                                                                                                                                                                                                     GYPGGKIIFIDTENTFRPDR------LRDIADRFNVDHDP------VLDNVL 189
                                                                                                                                                                                                                                               GGLGGKAVYIDTEGSFMVERVYQIAEGCIRDILEHFPHSHEKSSSVQKQLQPERFLADIY 143
                                                                                                                                                                                                                                                                                                                                      , 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P03017; 2REB.
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37707 MW;
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32.7%;
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Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                         EBBBDE57EB440402 CRC64;
                                                                                                                                                                                                                                                                                                                                      Mismatches
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.8e-20;
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Best Local
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                                                                  15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence up
30-MAY-2000 (Rel. 39, Last annotation
                                                                                                                    R51B_MOUSE
035719;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      microsporocytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tabata S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Embryophyta; Tracheop
Magnoliophyta; Liliopsida; Liliales; Liliaceae;
                                                                                                                                                  MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Meiosis; Cell cycle; ATP-binding; Nuclear protein.
NP_BIND 138 145 ATP (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kobayashi T., Kobayashi E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96051386; PubMed=7584025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Flower buds;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=4690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lilium longiflorum (Trumpet lily)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEIOTIC RECOMBINATION PROTEIN DMC1 HOMOLOG
                                  RAD51L1 OR RAD51B OR REC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Characterization of cDNAs induced in melotic prophase in
     Eukaryota;
                                                                                                                                                                                                                                                                                                                                                    197
                                                                                                                                                                                                                                                                                                                                                                                  135
                                                                                                                                                                                                                     312 LRKGKGEQRVCKIFDAPNLPESEAVFQITPGGVADA 347
                                                                                                                                                                                                                                                                                                                     192
                                                                                                                                                                                                                                                                                                                                                                                                                   153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 YVSGAQNAWDMFSDELSQKHITTGSGDLNDILGGGIHCKEVTEIGGVPGVGKTQLGIQLA 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: MAY PARTICIPATE IN MEIOTIC RECOMBINATION.
SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
SIMILARITY: STRONG TO OTHER EUKARYOTIC RECA-LIKE PROTEIN;
PROKARYOTIC RECA PROTEIN.
                  musculus (Mouse)
                                                    REPAIR PROTEIN RAD51 HOMOLOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YITGS ---- DVLLKRKSVIRITTGSQALDELLGGGIETLQITEAFGEFRSGKTQIAHTLC 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JC2214; JC2214
                                                                                                                                                                                                                                                 LH-WNGNERYAHLDKSPSLPVASAPYAVTGKGIRDA 283
                                                                                                                                                                                                                                                                                   RQQKLAQMLSRLTKIAEEFNVAVYMTNQVIADPGGGMFISDPKKPAGGHVLAHAATVRLM
                                                                                                                                                                                                                                                                                                                                                                                 PERFLADIYYFRICSYTEQIAVINYMEKFLREHKDVRIVIIDSVTFHFRQDFE---DLAL 191
                                                                                                                                                                                                                                                                                                                                                                                                                 VSTQLPVSMHGGNGKVAYIDTEGTFRPDRIVPIAERFGMD------ASAV----
                                                                                                                                                                                                                                                                                                                                                                                                                                              INVQIPVECGGLGGKAVYIDTEGSFMVERVYQIAEGCIRDILEHFPHSHEKSSSVQKQLQ 134
                                                                                                                                                                                                                                                                                                                RTRVLSGLSLKLMKIAKTYNLAVVLLNQVTTKFTEGSF---QLTLALGDSWSHSCTNRLI 248
                                                                                                                                                                                                                                                                                                                                                    ----LDNIIYARAYTYEHQYNLLLALAAKMSE-EPFRLLIVDSVIALFRVDFSGRGELAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D21821; BAA04845.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              349 AA;
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                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38272 MW;
     Chordata; Craniata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sato S., Hotta Y., Miyajima N., Tanaka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 313; DB 1
Pred. No. 1e-19;
                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDA444A1166DBEC6 CRC64;
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                                                                                       update)
                                                                                                                                       350
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      Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 349;
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15-JUL-1998 (Rel. 3
15-JUL-1998 (Rel. 3
15-JUL-1998 (Rel. 3
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DMC1_S
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SEQUENCE
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MGD; MGI:109436; Rad5111.

PROSITE; PS50162; RECA_2; 1.

DNA-binding; ATP-binding; Nuclear protein.

DNA-binding; ATP-binding; Nuclear protein.

ATP (POTENTI!)

ND BIND 108 115 ATP (POTENTI!)
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                                                                                    Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
                                                                                                                                                                   15-JUL-1998 (Rel. 36, Last sequence update) 15-JUL-1998 (Rel. 36, Last annotation updat MEIOTIC RECOMBINATION PROTEIN DMC1 HOMOLOG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entry of the Swiss Institute of Bioinformatics and the Entry of the Swiss Institute of Bioinformatics and the Entry of the Swiss Institute of Bioinformatics and the Entry of the Swiss Institute of Bioinformatics and the Entry of the Swiss Institute of Bioinformatics and the Entry of the Swiss Institute of Bioinformatics and the Entry of the Swiss Institute of Bioinformatics and the Entry of the Swiss Institute of Bioinformatics and the Entry of the Swiss Institute of Bioinformatics and the Entry of the Swiss Institute of Bioinformatics and the Entry of the Swiss Institute of Bioinformatics and the Entry of the Swiss Institute of Bioinformatics and the Entry of the Swiss Institute of Bioinformatics and the Entry of the Swiss Institute of Bioinformatics and the Entry of the Swiss Institute of Bioinformatics and the Entry of the Swiss Institute of Bioinformatics and the Entry of the Swiss Institute of Bioinformatics and the Entry of the Swiss Institute of Bioinformatics and the Entry of the Swiss Institute of Bioinformatics and the Entry of the Swiss Institute of Bioinformatics and the Entry of the Swiss Institute of Bioinformatics and the B
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NCBI_TaxID=3847;
[1]
                                                                                                                                         Glycine max (Soybean)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125 ATLPTSLGGLEGAVVYIDTESAFTAERLVEIAE-----SRFPQYFNTEEKLLLTSSRV 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                         341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROKARYOTIC RECA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GIRDAVSSNHKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VQIPVECGGLGGKAVYIDTEGSFMVERVYQIAEGCIRDILEHFP---HSHEK----SSSV 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QTAYELKTRRSAHLSPAFLSTTLCALDEALHGGVPCGSLTEITGPPGCGKTQFCIMMSVL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GL---VLQGHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLSEGTSGSSCLVAALGNTWGHCVNTRLILQYLDSERRQILIAKSPLAAFTSFVYTIKGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HLCRELTCEGLLQ-----RLESLEEEII-----
                                                                                                                                                                                                                                                                                                                  SOYBN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----DLALRTRVL-SGLSLKLMKIAKTYNLAVVLLNQVTTKF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --TEGSFQLTLALGDSWSHSCTNRLILHWNGNERYAHL-DKSPSLPVASAPYAVTGK 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 350 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           349
                                                                                                                                                                                                                                                        36, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 313; DB 1
Pred. No. 1e-19;
                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TP (POTENTIAL).
A57F547CA9CE6D65 CRC64;
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                                                                                                                                                                         ion update)
                                                                                                                                                                                                                                                                                                                  345 AA
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RESULT 12
RADA_METJA
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Best Local S
Matches 90
                                                                                                                                                                                                                                                                                                                                                                                                                                Q49593; Q58279;
01-NOV-1997 (Rel. 3
01-NOV-1997 (Rel. 3
15-DEC-1998 (Rel. 3
                                                                       SEQUENCE FROM N.A.

MEDILINE=96.51095; PubMed=8668545;

MEDILINE=96.51095; PubMed=8668545;

Sandler S.J., Satin L.H., Samra H.S., Clark A.J.;

Sandler S.J., Satin L.H., Samra H.S., Clark A.J.;

"recA-like genes from three archaean species with putative products similar to Rad51 and Dmcl proteins of the yeast Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U66836; AAB07025.1; -. HSSP; P03017; 2REB. PROSITE; PS50162; RECA_2; 1. PROSITE; PS50163; RECA_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the E the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Meiosis; Cell cycle; ATP-binding; Nuclear protein.
NP_BIND 134 141 ATP (POTENTIAL).
SEQUENCE
                                                Saccharomyces
Nucleic Acids
                                                                                                                                                                                                                                                                                                   Methanococcus
                                                                                                                                                                                                                                                                                                                          Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
                                                                                                                                                                                                                                                                                                                                                 Methanococcus jannaschii
                                                                                                                                                                                                                                                                                                                                                                          RADA OR MJ0869
                                                                                                                                                                                                                                                                                                                                                                                                       DNA REPAIR PROTEIN RADA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RADA_METJA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRKGKGEQRICKVFDAPNLPEAEAVFQITAGGIADA 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VSTQLPTNMRGGNGKVAYIDTEGTFRPDRIVPIAE-------RFGMD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RTRVLSGLSLKLMKIAKTYNLAVVLLNQVTTKFTEGSF---QLTLALGDSWSHSCTNRLI
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Pred. No. 1.2e-19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          685CB696F923BAB6 CRC64;
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Best Local S
Matches 92
                                                                                                                          DLH1_CANAL STANDARI
P50265;
01-OCT-1996 (Rel. 34, C
01-OCT-1996 (Rel. 34, I
01-NOV-1997 (Rel. 35, I
MEIOTIC RECOMBINATION F
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                                                                                                   DLH1
                                                                                                                                                                                                                                                                                                                    CANAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 273:1058-1073(1996).

-!- FUNCTION: PROBABLY INVOLVED IN DNA REPAIR AND IN HOMOLOGOUS RECOMBINATION AND REQUIRED FOR MEIOTIC RECOMBINATION.
-!- SIMILARITY: STRONG TO EUKARYOTIC RECA-LIKE PROTEIN; SOME, TO PROKARYOTIC RECA PROTEIN.
      Eukaryota; Fungi;
Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50162; RECA_2; 1. PROSITE; PS50163; RECA_3; 1.
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EMBL; U67531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE=96337999; PubMed=8688087;
                                                              Candida albicans (Yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA damage; DNA recombination; ATP-binding; DNA-binding, NP_BIND 136 143 ATP (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSFQLTLALGDSWSHSCTNRLILH-WNGNERYAHLDKSPSLPVASAPYAVTGKGIRD 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LVIVDSLTSTFRTEYIGRGKLAERQQKLGRHMATLNKLADIYNCVVIVTNQVAARPDALF
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                             Fungi;
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                                                                                                                             (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 35, Last annotation update)
(MBINATION PROTEIN DLH1 (DMC1 HOMOLOG).
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AAB98875.1; -.
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                                                                                                                                                                                                                                                                                            STANDARD;
   Ascomycota; mitosporic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20.4%; Score 312; DB 1; 31.0%; Pred. No. 1.3e-19; tive 47; Mismatches 106
   Saccharomycotina; Saccharomycetes; Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                            324
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Best Local :
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                                                                                                                                                   01-NOV-1997
01-NOV-1997
15-JUL-1998
Ferguson
Holloman
                                                                                                                                                                                             RA51_USTMA
Q99133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50162; RECA_2; 1.

PROSITE; PS50163; RECA_3; 1.

Meiosis; Cell cycle; ATP-binding; Nuclear protein.

MP_BIND 112 119

ATP (POTENTIAL).
MEDLINE=97225207; PubMed=9071580; Ferguson D.O., Rice M.C., Rendi NHOlloman W.K.;
                                                                               Eukaryota; Fungi; Bas
Ustilaginomycetidae;
                                                                                                            Ustilago maydis
                                                                                                                                       DNA REPAIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- FUNCTION: REQUIRED FOR MEIOTIC RECOMBINATION, SYNAPTO FORMATION AND CELL CYCLE PROGRESSION (BY SIMILARITY).
-1- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
-1- SIMILARITY: STRONG TO OTHER EUKARYOTIC RECA-LIKE PROT PROKARYOTIC RECA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     meiosis-specific gene DMC1.";
Genetics 143:769-776(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Diener A.C., Fink G.R.; "DLH1 is a functional Candida albicans homologue
                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                         261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Ew European Bloinformatics Institute. There are no restr by non-profit institutions as long as its content
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                                                                                                                                                                                                                                                                                                                                     DYNIAVFLTNQVQS--DPGASALFAAADGRKPVGGHVLAHASATRILLRKGRGEERVAKL
                                                                                                                                                                                                                                                                                                                                                             TYNLAVVLLNQVTTKFTEGSFQLTLAL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HITTGSKQFDEILGGGIQSMSITEVFGEFRCGKTQLCHTLCVAAQLPTDMGGGEGRVAYI 145
                                                                                                                                                                                                                                                                                                                                                                                                                    EQIAVINYMEKFLREHKDVRIVIIDSVTFHFRQDFE---DLALRTRVLSGLSLKLMKIAK
                                                                                                                                                                                                                                                                                                                                                                                                                                               DTEGTFRPDRIRSIAERYGVDADIC----------------LENISYARALNSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DTEGSFMVERVYQIAE--GCIRDILEHFPHSHEKSSSVQKQLQPERFLADIYYFRICSYT 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U39808; AAC49400.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87;
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                                                                                                                                       PROTEIN
                                                                                                                                                 7 (Rel. 35,
7 (Rel. 35,
8 (Rel. 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              324 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                               (Smut fungus).
i; Basidiomycota; Usi.idae; Ustilaginales;
                                                                                                                                                                                                           STANDARD;
                                                                                                                                       RAD51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35281 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      license agreement (See http://www.isb-sib.ch/announce/
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33.2%;
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                                                                                                                                                                              Created)
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          Rendi M.H.,
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                                                                                                                                                                                                                                                                               322
                                                                                                                                                                                                                                                                                                         282
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Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95CD769514D9CF82 CRC64;
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                                                                                            Ustilaginomycetes;
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                                                                               Ustilaginaceae;
                                                                                                                                                                update)
                                                                                                                                                                                                           339
           Kotani H.,
                                                                                                                                                                                                                                                                                                                                                             -GDSWSHSCTNRLILH-WNGNERYAHL
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Best Loc
Matches
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042634; 042880;
05-DEC-1998 (Rel
01-OCT-2000 (Rel
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SEQUENCE
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PROSITE; PS50163; RECA_3; 1.

DNA damage; DNA repair; ATP-binding; DNA recombination.

NP_BIND 127 134 ATP (POTENTIAL).

NP_BIND 127 134 ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Genetics 145:243-251(1997).

-i- FUNCTION: REQUIRED BOTH FOR RECOMBINATION AND FOR THE DNA DAMAGE CAUSED BY X-RAYS (BY SIMILARITY).
recombination.";
Nucleic Acids Re
                                                ranaka S., Nojima H.;
rDmcl of Schizosaccharomyces pombe plays
                                                                                  Fukushima K., Tanaka
Tanaka S., Nojima H.;
                                                                                                                                                                                                                                                                        Schizosaccharomycetales;
                                                                                                                                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces pombe (Fission yeast)
                                                                                                                                                                                                                                                                                                                                                                DMC1 OR DMP1 OR SPAC8E11.03C
                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (Rel. 40, Last annotation MEIOTIC RECOMBINATION PROTEIN DMC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U62484; AAC61878.1; -.
                                                                                                                                     SEQUENCE FROM N.A., AND FUNCTION. MEDLINE=20368631; PubMed=10908327;
                                                                                                                                                                                                                     NCBI_TaxID=4896;
                                                                                                                                                                                                                                                 Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000445; -. Pfam; PF00633; HHH; 1.
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(Rel. 40, Last sequence update)
(Rel. 40, Last annotation updat
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                                                                                                            Y., Nabeshima
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                                                                                                         Yoneki T., Tougan T.
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Best Local Similarity
Matches 82; Conserv
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MP_BIND
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Q -> K (IN REF. 2).
SEQUENCE
332 AA; 36408 MW; 86B73EAA491F7B02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AB008545; BAA28671.1; -. EMBL; D64035; BAA23984.1; -. EMBL; AL021817; CAA17024.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50162; RECA_2; 1. PROSITE; PS50163; RECA_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: NUCLEAR.
-!- SIMILARITY: STRONG TO OTHER EUKARYOTIC RECA-LIKE PROTEIN; SOME, TO PROKARYOTIC RECA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         McLean J., Harris D., Wood V., Barrell B.G., Rajandream M.A.; Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: REQUIRED FOR MEICTIC RECOMBINATION AND CELL CYCLE PROGRESSION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases. [3]
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SEQUENCE FROM N.A.
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                                                                                                                                           184 VSRAYNSEQQMEYITKLGTIFAEDGQYRLLIVDSIMALFRVDYSGRGELSERQQKLNIML
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                                                                                                      201 LKLMKIAKTYNLAVVLLNQVTTKFTEGSFQLTLALGDS------WSHSCTNRLILH-WN 252
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GEERVAKLNDSPDMPEAECSYVITPGGIAD 330
                                                                                                                                                                 YFRICSYTEQIAVINYMEKFLREHKDVRIVIIDSVTFHFRQDFE---DLALRTRVLSGLS 200
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                                 GNERYAHLDKSPSLPVASAPYAVTGKGIRD 282
                                                                   ARLNHISEEFNVAVFVTNQVQ----ADPGAAMMFASNDRKPVGGHVMAHASATRLLLRKGR 300
                                                                                                                                                                                                                     GGAEGKVAFIDTEGTFRPDRIKAIAE----
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                                                                                                                                                                                                                     -RFGVDADQAMENII 183
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                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Search completed: October 1, 2001, 16:29:24
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Post-processing: Minimum Match 0%
Maximum Match 100%
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44 14/.5 45 133	43 148								35 206				31 242	
8.7			12.2	12.4	13.0	13.0	13.0	13.1	13.5	13.5	14.1	15.8	15.8	16.7
458	285	350	225	234	516	228	212	239	221				353	529
2 0	) E	2 T	2 T	1 D	2 T	1 E	1 G	2 C	1 H			2 J(	2 D	2 н.
866116	H86212	T43680	F43936	D69093	F49422	E71232	G64331	c75199	н69511	A84319	16872	JQ1275	D84686	171450
DNA repair protein	hypothetical prote	DNA repair protein	probable DNA repai	DNA repair protein	RAD57 related prot	probable DNA repai	DNA repair protein	recombinase PAB227	DNA repair protein	DNA repair protein	DNA repair protein	RAD57 protein - ye	probable RAD51B-li	

## ALIGNMENTS

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487
A;Accession: F84888

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999

probable RAD51C-like DNA repair protein [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001

C; Accession: F84888

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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-332 <STO>
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                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
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                                                                                                                                                                                                            119
                                                                                                                                                                      139 LADIYYERICSYTEQIAVINYMEKFLREHKDVRIVIIDSVTFHFRQDFEDLALRTRVLSG 198
298
                    259 HLDKSPSLPVASAPYAVTGKGIRDAVSSNHKRARV 293
                                                                  199 LSLKLMKIAKTYNLAVVLLNQVTTKFTEGSFQLTLALGDSWSHSCTNRLILHWNGNERYA 258
                                                                                                                                                                                                                                   79 IPVECGGLGGKAVYIDTEGSFMVERVYQIAEGCIRDILEHFPHSHEKSSSVQKQLQPERF 138
                                                                                                                                                                                                                                                                               59 AKNAWDMLHEEESLPRITTSCSDLDNILGGGISCRDVTEIGGVPGIGKTQIGIQLSVNVQ 118
                                                                                                                                                                                                                                                                                                 19 AQNAWDMFSDELSQKHITTGSGDLNDILGGGIHCKEVTEIGGVPGVGKTQLGIQLAINVQ 78
                                                                                                                                                                                                                                                                                                                                                   Local Similarity
mes 183; Conserv
                                                                                                                                      YIDKSPSLPSASASYTVTSRGLRNS-SSSSKRVKM
                                                                                                                                                                                                           IPRECGGLGGKAIYIDTEGSFMVERALQIAEACVEDMEEYTGYMHKHFQANQVQMKPEDI 178
                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                   64.6%; Score 988; DB 2; Length 332; 66.5%; Pred. No. 2.9e-77; tive 51; Mismatches 39; Indels
     331
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probable radA protein APE0119 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 20-Jun-2000

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A;Gene:
C;Superf
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A;Title: recA-like genes from three archavire from the muber: 871093; MUID:96251095
A;Accession: 871093
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C;Species: Sulfolobus solfataricus
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change
C;Accession: S71093
                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references:
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-324 <SAN>
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C;Superfamily: yeast DNA repair protein RAD51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Experimental source: strain K1 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-319 <KAW>
A;Cross-references: DDBJ:AP000058; NID:g5103388; PIDN:BAA79030.1; PID:g5103509
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R;Kawarabayasi, Y; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takal awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kudoh, Res. 6, 83-101, 1999
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
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A;Accession: D72766
                                                                                                                                                                                                                             Query Match
Best Local
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Best Local
                   119
                                                   65 GKTQLGIQLAINVQIPVECGGLGGKAVYIDTEGSFMVERVYQIAEGCIRDILEHFPHSHE 124
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                                                                                                                                                                                                                                                                                                                                                radA
                                                                                                                                                  QKYVSGAQNAWD------MFSDELSQKHITTGSGDLNDILGGGIHCKEVTEIGGVPGV 64
            GKTQLCHQLSVNVQLPPEKGGLSGKAVYIDTEGTFRWERIENMAKALGLDI
                                                                                                      QKIIKEARDALDIRFKTALEVKKERMNVKKISTGSQALDGLLAGGIETRTMTEFFGEFGS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EFPGRENLAMRQQLLNRHLHQLMRLADIFNVAVVITNQVMARPDVFYGDPTQAVGGHVLG 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----GLDPDEVMKNIYWIRAINSHHQIAIVDKLFTMVK-NDNIKLVVVDSVTSHFRA 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KSSSVQKQLQPERFLADIYYFRICSYTEQIAVINYMEKFLREHKDVRIVIIDSVTFHFRQ 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GKTQICHQLSVNVQLPEDKGGLEGKAVYVDTEGTFRWERIEQMARGV-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QKIVDAAREALNIDFKTAYDLKIESMNIKKITTGSRNLDELLGGGIETKTITELFGEFGS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QKYVSGA-----QNAWDMFSDELSQKHITTGSGDLNDILGGGIHCKEVTEIGGVPGV 64
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97; Conser
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                                                                                                                                                                                                                                                                                                                                                                                     EMBL: U45310; NID: g1378035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from three archaean species with putative
                                                                                                                                                                                                                         25.3%;
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                                                                                                                                                                                                                      Score 387.5; DB 2; Pred. No. 1e-25;
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Pred. No. 3e-28;
                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H.S.; Clark, A.J.
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                                                                                                                                                                                                                                                                                                                                                                                  PIDN:AAC44123.1; PID:g1378036
                                                                                                                                                                                                   93;
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                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                            Length 324;
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R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: fu A;Reference number: A69000; MUID:98037514
                                                                                                                                           C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999
C;Accession: A69051
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                                                                                                                                                                                                                                            A69051
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Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch A;Reference number: A69250; MUID:98049343
A;Accession: A69374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-337 <KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
Nature 390, 364-370, 1997
Nature 390, 364-370, 1997
Nature 390, 364-370, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA repair protein RAD51 (radA) homolog - Archaeoglobus fulgidus C;Species: Archaeoglobus fulgidus C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999
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        284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 VSGAQNAWDMFSDELSQKHITTGSGDLNDILGGGIHCKEVTEIGGVPGVGKTQLGIQLAI 75
                                                      HSCTNRLILHWNGNE-RYAHLDKSPSLPVASAPYAVTGKGIRDAVSSNHKRAR 292
                                                                                                                                                                                                                      NEVLKNIYVAQAYNSNHQMLLVDNAKELAEKLKKEGRPVRLIIVDSLMSHFRAEYVGRGT 230
                                                                                                                                                                                                                                                                      ERFLADIYYFRICSYTEQIAVIN----YMEKFLREHKDVRIVIIDSVTFHFRQDF---ED 188
HTATFRIYLKKGKDDLRIARLIDSPHLPEGEAIFRVTERGIEDAEEKDKKKRK
                                                                                                            LADRQQKLNRHLHDLMKFGELYNAAIVVTNQVMAR-----PDVLFGDPTKPVGGHIVA
                                                                                                                                                             LALRTRVLSGLSLKLMKIAKTYNLAVVLLNQVTTKFTEGSFQLTLALGDSW------S 240
                                                                                                                                                                                                                                                                                                                                                                                NVQIPVECGGLGGKAVYIDTEGSFMVERVYQIAEGCIRDILEHFPHSHEKSSSVQKQLQP 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KSSSVQKQLQPERFLADIYYFRICSYTEQIAVINYMEKFLREHKDVRIVIIDSVTFHFRQ 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HVPGIRIQLKKSRGNRRIARVVDAPHLPEGEVVFALTEEGIRDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DF---EDLALRTRVLSGLSLKLMKIAKTYNLAVVLLNQVTTKFTEGSFQLTLAL-GDSWS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----DNVMNNIYYIRAINTDHQIAIVDDLQELVSKDPSIKLIVVDSVTSHFRA 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EYPGREILAVRQQKLNKHLHQLTRLAEVYDIAVIITNQVMARPDMFYGDPTVAVGGHTLY 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23.2%; Score 354.5; DB 2 32.4%; Pred. No. 7.5e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 337;
                                                                                                                                                                                                                                                                                                                               -- KGLDG 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PID: g264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6;
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A;Accession: A69051
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Residues: 1-311 <MTH>
A;Cross-references: GB:AE000901; GB:AE000666; NID:g2622486; PIDN:AAB85860.1; FA,Experimental source: strain Delta H C;Genetics:
A;Genetics:
A;Genetics:
A;Genetiming: yeast DNA repair protein RAD51
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                                                                                                                                                                                                                                                                                                                     A;Gene: radA; PABULD4
C;Superfamily: yeast DNA repair protein RAD51
                                                                                                                                                                                                                                                                                                                                                                        A; Experimental source: strain Orsay C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA repair protein rad51 (rada) PAB0164 - Pyrococcus abyssi (strain Orsay) C;Species: Pyrococcus abyssi C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA A; Residues: 1-356 <KAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: A75001
A; Recession: F75214
                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AJ248283; GB:AL096836; NID:g5457433; PIDN:CAB49165.1; PID:g54576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, July 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession:
                                                                                                                                                                                                                                        Query Match
Best Local s
Matches 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
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               195
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                                                     116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     266 VLGHAATYRIWLKKGLAGKRIARLVDSPHLPEGECVFKITTAGIVD 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106
                                                                                        141 TEVFGEFGSGKTQLAHTLAVMVQLPPEEGGLNGSVIWIDTENTFRPERIREIAK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRAEYVGREALATRQQKLNQHLHTLQNIANTYNAAVFVTNQVQARPDAFFGSPTKAIGGH 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRQDF----EDLALRTRVLSGLSLKLMKIAKTYNLAVVLLNQVTTKFTEGSFQLTLALGDS 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SHEKSSSVQKQLQPERFLADIYYFRICSYTEQIAVINYMEKFLREHKDVRIVIIDSVTFH 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FGSGKSQLSHELAVTVQLPEERGGLDAEAVFIDTENTFRPERIEQIANAF------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GVAEKVIEAARRAEKIDFETAFDVMERRKDVGRITTGSKALDELIGGGIETQAITEVFGE 105
                                                 LEHFPHSHEKSSSVQKQLQPERFLADIYYFRICSYTEQIAVINYMEKFLRE----HKDVR 171
                                                                                                                                                                 AGISEGAALKIIQAARKAANLGTFMRADEYLKKRESIGRISTGSKSLDKLLGGGIETQAI 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -WSHSCTNRLILHWN-GNERYAHLDKSPSLPVASAPYAVTGKGIRD 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGVGKTQLGIQLAINVQIPVECGGLGGKAVYIDTEGSFMVERVYQIAEGCIRDILEHFPH 121
                                                                                                              TEIGGVPGVGKTQLGIQLAINVQIPVECGGLGGKAVYIDTEGSFMVERVYQIAEGCIRDI 115
                                                                                                                                                                                                   SGSRNGPQQKYVSGAQNAWD----MFSDELSQK-----HITTGSGDLNDILGGGIHCKEV 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96;
                                                                                                                                                                                                                                          97; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genoscope
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         · ELDLEEVLNKIHIARAFNSSHQILMAEKVNELIQEGKNIRLVIVDSLTAH
               -NRGLDPDEVLKHIYVARAFNSNHQMLLVQQAEDKIKELLNTDKPVK 240
                                                                                                                                                                                                                                                          22.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46;
                                                                                                                                                                                                                                                            Score 345; DB 2; Pred. No. 5.3e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 352.5;
Pred. No. le
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111;
                                                                                                                                                                                                                                            107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            insights
                                                                                                                                                                                                                                                                              Length 356;
                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33;
                                                                                                                                                                                                                                            44;
                                                                                                                                                                                                                                          Gaps
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                                                                                          194
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                                                                                                                                                                                                                                          8
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дb
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A;Cross-references: S
A;Map position: 5R
A;Introns: 44/3
C;Function:
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A:Reference number: S30812
A:Accession: S30857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, December 1994 A; Description: The sequence of S. cerevisiae cosmids A; Reference number: S50682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:M87549; NID:g171400; R;Kobayashi, T.; Hotta, Y.; Tabata, S. Mol. Gen. Genet. 237, 225-232, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell 69, 439-456, 1992
A; Title: DMC1: a meiosis specific yeast homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Saccharomyces cerevisiae
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993
C;Accession: A38214, S30276, S30857; S50682
R;Bishop, D.K.; Park, D.; Xu, L.; Kleckner, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                meiosis-specific recombination protein DMC1 [validated] N;Alternate names: protein YER179w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Description: DMC1 is involved in reciprocal recombination during meiosis C;Superfamily: yeast DNA repair protein RAD51 C;Keywords: purine nucleotide binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-334 <MUL>
A;Cross-references: GB:U18922; EMBL:L11229; NID:g603405; PIDN:AAB64706.1; PID:g603420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Title: Isolation and characterization of a yeast gene A; Reference number: $30275; MUID:93204898 A; Accession: $30276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-334 <BIS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: A38214; MUID:92257586
A; Accession: A38214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-334 <DIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Dietrich, F.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-334 < KOB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: SGD: DMC1; ISC2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: S50682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:U18922; NID:g603405; PIDN:AAB64706.1; PID:g603420;
                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                      Best
  196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 LIVDSLTSHFRSEYIGRGALAERQQKLAKHLADLHRLANLYEIAVFVTNQVQARPDAFF 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      155 AVINYMEKFLREHKDVRIVIIDSVTFHFRQDF---EDLALRTRVLSGLSLKLMKIAKTYN 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 GDPTRPIG---GHILAHSATLRVYLRKGKGGKRVARLIDAPHLPEGEAVFRITEKGIED
                                                                                                     156
                                                                                                                                                     95
                                                                                                                                                                                                        96
                                                                                                                                                                                                                                                      35 ITTGSGDLNDILGGGIHCKEVTEIGGVPGVGKTQLGIQLAINVQIPVECGGLGGKAVYID
                                                                                                                                                                                                                                                                                                                                      Local
ELVEQLGEEL-SSGDYRLIVVDSIMANFRVDYCGRGELSERQQKLNQHLFKLNRLAEEFN
                                                                                                                                                                                                      LSTGSKQLDSILGGGIMTMSITEVFGEFRCGKTQMSHTLCVTTQLPREMGGGEGKVAYID 155
                                                                                                                                                TEGSFMVERVYQIAEGCIRDILEHFPHSHEKSSSVQKQLQPERFLADIYYFRICSYTEQI 154
                                                                                                                                                                                                                                                                                                              87;
                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SC2; MIPS:YER179w
SGD:S0000981; MIPS:YER179w
                                                                                                                                                                                                                                                                                                                                      22.0%;
33.5%;
                                                                                                                                                                                                                                                                                                         46;
                                                                                                                                                                                                                                                                                                                                      Score 337; DB 2;
Pred. No. 2.3e-21;
                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                        -YELDPESCLANVSYARALNSEHQM
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                                                                                                                                                                                                                                                                                                                                                              Length 334;
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    yeast (Saccharomyces

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                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                        195
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R;Sato, S.; Kobayashi, T.; Hotta, Y.; Tabata, S.

DNA Res. 2, 147-150, 1995

A;Title: Characterization of a mouse recA-like gene specifically expressed in te.

A;Reference number: JC4191

A;Accession: JC4191

A;Molecule type: mRNA

A;Residues: 1 -340 <SANT>

A;Cross-references: DDBJ:D58419; NID:g961475; PIDN:BAA09590.1; PID:g961476

A;Experimental source: testis

R;Habu, T.; Taki, T.; West, A.; Nishimune, Y.; Morita, T.

Nucleic Acids Res. 24, 470-477, 1996

A;Title: The mouse and human homologs of DMC1, the yeast meiosis-specific homolo

A;Reference number: S62353

A;Accession: S62353; MUID:g6173646

A;Residues: 1-340 <HABb>
A;Residues: 1-340 <HABb>
A;Cross-references: EMBL:D64107; NID:g987666; PIDN:BAA10969.1; PID:g1321647

C;Comment: This protein participates in the meiotic recombination process during
C;Genetics:
A;Gene: MmLim15

C;Superfamily: yeast DNA repair protein RAD51

C;Keywords: nucleotide binding; P-loop; spermatogenesis; testis
E;126-133/Region: nucleotide-binding motif A (P-loop)
F;219-224/Region: nucleotide-binding motif B
meiosis-specific recombination protein DMC1 - N;Alternate names: meiosis-specific RecA-like C;Species: Homo sapiens (man)
                                                                                                                                                                                                        Qγ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20
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                                                                                                                                                               DSPEMPENEATFAITAGGIGDA
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                                                                                                                                                                                                                                                       YNVAVEVTNQMT---ADPGATMTFQADPKKPIGGHILAHASTTRISLRKGRGELRIAKIY
                                                                                                                                                                                                                                                                                                                                             MELLDYVAAKFHEEAGIFKLLIIDSIMALFRVDFSGRGELAERQQKLAQMLSRLQKISEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DTEGSFMVERVYQIAEGCIRDILEHFPHSHEKSSSVQKQLQPERFLADIYYFRICSYTEQ 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HITTGSQEFDKLLGGGIESMAITEAFGEFRTGKTQLSHTLCVTAQLPGTGGYSGGKIIFI 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HITTGSGDLNDILGGGIHCKEVTEIGGVPGVGKTQLGIQLAINVQIPVECGGLGGKAVYI 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VAVFLTNQVQS--DPGASALFASADGRKPIGGHVLAHASATRILLRKGRGDERVAKLQDS
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                                                                                                                                                                                                                                                                                                                                                                                        IAVINYM-EKFLREHKDVRIVIIDSVTFHFRQDFE---DLALRTRVLSGLSLKLMKIAKT 209
                                                                                                                                                                                                                                                                                                                                                                                                                                        DTENTFRPDR-----LRDIADRFNVDH------EAVLDNVLYARAYTSEHQ
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Pred. No. 2.1e-19;
3; Mismatches 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -GDSWSHSCTNRLILH-WNGNERYAHLDKS
                                                                                                                                                                                                                                                                                                -GDSWSHSCTNRLILH-WNGNERYAHLD 261
                   protein;
                                             human
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R;Kobayashi, T.; Kobayashi, E.; Sato, S.; Hotta, DNA Res. 1, 15-26, 1994
A;Title: Characterization of cDNAs induced in me:
A; Molecule type: mRNA
A; Residues: 1-349 < KOB>
                                            A; Status: preliminary
                                                                     A; Reference number: PC2136; A; Accession: JC2214
                                                                                                                                                                                    C; Accession: JC2214
                                                                                                                                                                                                             C; Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 20-Jun-2000
                                                                                                                                                                                                                                        hypothetical 38.3K protein, LIM15 - trumpet lily C; Species: Lilium longiflorum (trumpet lily)
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C;Keyords: DNA binding; melosis; nucleotide binding;
F;126-133;Region: nucleotide-binding motif A (P-loop)
F;219-223/Region: nucleotide-binding motif B
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A;Residues: 1-36,'I',38-182,'P',184-340 <SAT>
A;Cross-references: DDBJ:D63882; NID:g1066000; PIDN:BAA09932.1; PID:g1066001
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A;Title: Expression profiles of a human gene identified
A;Reference number: JC4333; MUID:96127532
A;Accession: JC4333
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                                                                                                                                                                                                                                                                                                                                                                                                                                  NGNERYAHLDKSPSLPVASAPYAVTGKGIRDA
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                                                                                           MUID:96051386
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Pred. No. 2.
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                                                                                                                                                              Y.; Miyajima,
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A;Cross-references: DDBJ:D21821; NID:g431167; C;Superfamily: yeast DNA repair protein RAD51

PIDN: BAA04845.1;

PID: 9431168

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C;Superfamily: yeast DNA repair protein RAD51
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C;Function:
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A; Residues: 1-345 <HAD>
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submitted to the EMBL Data Library, August 1996
A;Description: RecA like gene from soybean.
A;Reference number: Z16485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RecA/Rad51/DMC1-like protein - soybean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
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  308
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                                                                                                                                                                                                                                                                                                                                                                       93
                                                                                                                                                                                                                                                                                                                                                                                                                15 YVSGAQNAWDMFSDELSQKHITTGSGDLNDILGGGIHCKEVTEIGGVPGVGKTQLGIQLA 74
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                                                                                                                                                                                                                                                                                                                   75 INVQIPVECGGLGGKAVYIDTEGSFMVERVYQIAEGCIRDILEHFPHSHEKSSSVQKQLQ 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 YVSGAQNAWDMFSDELSQKHITTGSGDLNDILGGGIHCKEVTEIGGVPGVGKTQLGIQLA 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
FRKGKGEQRICKVFDAPNLPEAEAVFQITAGGIADA 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YITGS----DVLLKRKSVIRITTGSQALDELLGGGIETLQITEAFGEFRSGKTQIAHTLC 152
                                           LH-WNGNERYAHLDKSPSLPVASAPYAVTGKGIRDA 283
                                                                                                                                                                               PGAVLDNIIYARAYTYEHQYNLLLGLAAKMSE-EPFRLLIVDSVIALFRVDFSGRGELAD 247
                                                                                                                                                                                                                                                                          VSTQLPTNMRGGNGKVAYIDTEGTFRPDRIVPIAE------RFGMD 188
                                                                                                                                                                                                                                                                                                                                                                   YITGS----DALLKRKSVIRITTGSQALDELLGGGVETSAITEAFGEFRSGKTQLAHTLC 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RQQKLAQMLSRLTKIAEEFNVAVYMTNQVIADPGGGMFISDPKKPAGGHVLAHAATVRLM 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RTRVLSGLSLKLMKIAKTYNLAVVLLNQVTTKFTEGSF---QLTLALGDSWSHSCTNRLI 248
                                                                                        RQQKLAQMLSRLIKIAEEFNVAVYMTNQVISDPGGGVFVTDPKKPAGGHVLAHAATVRLM
                                                                                                                                 RTRVLSGLSLKLMKIAKTYNLAVVLLNQVTTKFTEGSF---QLTLALGDSWSHSCTNRLI 248
                                                                                                                                                                                                                          PERFLADIYYFRICSYTEQIAVINYMEKFLREHKDVRIVIIDSVTFHFRQDFE---DLAL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LRKGKGEQRVCKIFDAPNLPESEAVFQITPGGVADA 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LH-WNGNERYAHLDKSPSLPVASAPYAVTGKGIRDA 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PERFLADIYYFRICSYTEQIAVINYMEKFLREHKDVRIVIIDSVTFHFRQDFE---DLAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INVQIPVECGGLGGKAVYIDTEGSFMVERVYQIAEGCIRDILEHFPHSHEKSSSVQKQLQ 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20.5%; Score 313; DB 2; Length 349; 33.3%; Pred. No. 2.9e-19; tive 48; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 312; DB 2;
Pred. No. 3.4e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---ASAV---- 196
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RESULT 12 E64408 DNA repair

repair protein

radA -

Methanococcus

jannaschii

The Caenorhabditis elegans RAD51 homolog is transcribed into two alternative

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A;Cross-references: EMBL:AB011382; NID:g2913896; PIDN:BAA24982.1; PID:g2913897 R;Rinaldo, C.; Ederle, S.; Rocco, V.; La Volpe, A. Mol. Gen. Genet. 260, 289-294, 1998
                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-357 <TAK>
                                                                                                                                                                                                                                                                                                                        R;Takanami, T.; Sato, S.; Ishihara, T.; Katsura, I.; Takahashi, H.; Higashitani, A. DNA Res. 5, 373-377, 1998
A;Title: Characterization of a Caenorhabditis elegans recA-like gene Ce-rdh-1 involve A;Reference number: Z21672; MUID:99156232
A;Accession: T37305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Caenorhabditis elegans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C;Accession: T37305; T43059
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A;Title: recA-like genes from three archaean species with A;Reference number: S71093; MUID:96251095
A;Accession: S71095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus ja A;Reference number: A64300; MUID:98337999
A;Accession: E64408
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C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Ju1-2000
C;Accession: E64408; S71095; S71096
C;Accession: E64408; S71095; S71096
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Bla; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, R.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, R.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, R.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, R.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, R.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, R.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, R.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, R.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, R.; Merrick, J.M.; Glodek, R.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, R.; Merrick, J.M.; Glodek, R.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, R.; Merrick, J.M.; Glodek, R.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, R.; Merrick, J.M.; Glodek, R.; Reich, R.; Merrick, R.; Merr
                                                                                                                                                                                                                                                                         A; Status: preliminary; translated from GB/EMBL/DDBJ
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C; Superfamily: yeast DNA repair protein RAD51
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C;Genetics:
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A; Residues: 1-352 <BUL>
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A; Residues: 33-352 <SA2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 VPGVGKTQLGIQLAINVQIPVECGGLGG------KAVYIDTEGSFMVERVYQIAEGC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93 LGFKSGT-----EVLSQRKNIW------KLSTGSKNLDEILGGGLESQSVTEFAG 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LVIVDSLTSTFRTEYIGRGKLAERQQKLGRHMATLNKLADIYNCVVIVTNQVAARPDALF 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IRDILEHFPHSHEKSSSVQKQLQPERFLADIYYFRICSYTEQIAVINYMEKFLREHKDVR 171
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Pred. No. 3.5e-19;
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Appochetical protein Y43C5A.6 - Caenorhabditis elegans
C;Species; Caenorhabditis elegans
C;Species; Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C;Accession: T26822
R;White, S:
submitted to the EMBL Data Library, June 1998
A;Reference number: Z20272
A;Accession: T26822
A;Accession: T26822
A;Accession: T26822
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-391 <WIL>
A;Residues: 1-391 <WIL>
A;Cross-references: EMBL:AL023838; PIDN:CAA19500.1; GSPDB:GN00022; CESP:Y43C5A.6
A;Experimental source: clone Y43C5A
A;Genetics:
A;Genetics:
A;Genes: CESP:Y43C5A.6
A.Man, Nosetics:
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A;Accession: T43059
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-357 <RIN>
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A;Introns: 31/3; 125/3; 174/3; 227/2; 258/1; 350/2
C;Superfamily: yeast DNA repair protein RAD51
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Best Local Similarity
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252 ALIIRAGAMMSESR-YAVVIVDCATAHFRNEYTGRGDLAERQMKLSAFLKCLAKLADEYG
                                        155 AVINYMEKFLREHKDYRIVIIDSVTFHFRQDFE----DLALRTRVLSGLSLKLMKIAKTYN 211
                                                                                       212 TNATFRPERIIAIAQ-----
                                                                                                                                                                               152 IRTGSASLDRLLGGGIETGSITEVYGEYRTGKTQLCHSLAVLCQLPIDMGGGEGKCMYID 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95
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                                                                                                                                95 TEGSFMYERVYQIAEGCIRDILEHFPHSHEKSSSVQKQLQPERFLADIYYFRICSYTEQI 154
                                                                                                                                                                                                                          35 ITTGSGDLNDILGGGIHCKEVTEIGGVPGVGKTQLGIQLAINVQIPVECGGLGGKAVYID 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LPVASAPYAVTGKGIRDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VAVIITNQVVAQVDGGASMFQADAKKPIGGHIIAHMSTTRLYLRKGKGENRVAKMVQSPN 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAVVLLNQVTTKFTEGS--FQLTLAL---GDSWSHSCTNRLILH-WNGNERYAHLDKSPS 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIIRAGAMMSESR-YAVVIVDCATAHFRNEYTGRGDLAERQMKLSAFLKCLAKLADEYG 276
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                                                                                                                                                                                                                                                                         87; Conservative
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                                                                                                                                                                                                                                                                                            20.2%; Score 309; DB 2; Length 391; 33.7%; Pred. No. 7.3e-19;
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Pred. No. 6.5e-19;
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                                                                                          -- RYNMDSAHVLENTAVARAYNSEHLM
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R:Diener, A.C.; Fink, G.R. Genetics 143, 769-776, 1996
A;Title: DLH1 is a functional Candida albicans homologue of the meiosis-specific gene A;Reference number: S70390; MUID:96363911
A;Accession: S70390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Candida albicans
C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 29-Sep-1999
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C;Superfamily: yeast DNA repair protein RAD51
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C;Species: Candida albicans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:U39808; NID:g1145715; PIDN:AAC49400.1; PID:g1145716
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A; Residues: 1-324 <DIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          212 LAVVLLNQVTTKFTEGS--FQLTLAL---GDSWSHSCTNRLILH-WNGNERYAHLDKSPS
301
                                                                                     243
                                                                                                                             209 TYNLAVVLLNQVTTKFTEGSFQLTLAL------GDSWSHSCTNRLILH-WNGNERYAHL 260
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nes 87; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DLH1
QDSPNMPEKECVYVIGEGGIKD 322
                                      DKSPSLPVASAPYAVTGKGIRD 282
                                                                                     DYNIAVFLTNQVQS--DPGASALFAAADGRKPVGGHVLAHASATRILLRKGRGEERVAKL 300
                                                                                                                                                                        HQIELVEQLGNELAE-GTFRLLIVDSIMACFRVDYSGRGELNERQQKLNQHLSNLTRVAE 242
                                                                                                                                                                                                                     EQIAVINYMEKFLREHKDVRIVIIDSVTFHFRQDFE---DLALRTRVLSGLSLKLMKIAK 208
                                                                                                                                                                                                                                                                  DTEGTFRPDRIRSIAERYGVDADIC---------LENISYARALNSE 183
                                                                                                                                                                                                                                                                                                             DTEGSFMVERVYQIAE--GCIRDILEHFPHSHEKSSSVQKQLQPERFLADIYYFRICSYT 151
                                                                                                                                                                                                                                                                                                                                                        HITTGSKQFDEILGGGIQSMSITEVFGEFRCGKTQLCHTLCVAAQLPTDMGGGEGRVAYI 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  38;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 304; DB 2;
Pred. No. 1.5e-18;
8; Mismatches 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                       99;
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Search completed: October 1, 2001, 16:28:37 Job time: 70 sec

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Maximum DB
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seq length:
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Gapop 10.0 , Gapext 1.0
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1474
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/SIDS1/gcgdata/geneseq/geneseqn/NA1981.DAT:*
/SIDS1/gcgdata/geneseq/geneseqn/NA1981.DAT:*
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/SIDS1/gcgdata/geneseq/geneseqn/NA1984.DAT:*
/SIDS1/gcgdata/geneseq/geneseqn/NA1984.DAT:*
/SIDS1/gcgdata/geneseq/geneseqn/NA1986.DAT:*
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## ALIGNMENTS

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WPI; 2001-016092/02.
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                                                                                       Mahajan PB,
                                                                                                                                                                                                                                                                          05-MAY-1999;
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/product= "Maize RAD51 orthologue protein #1"
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amplification primers recombination or RAD51 polynucleotides, useful for e.g. controlling tion or transformation efficiency in plants, or as p tion primers for detecting, quantifying or isolating probes gene or

Claim 1; Page 68-69; 76pp; English.

The present sequence is a maize RAD51 orthologue #1 cDNA. RAD51 is one CC of the genes of the RAD52 epistasis group that is involved in double strand breaks (DSBs) repair by homologous recombination. Control of CC homologous recombination by modulating RAD51 is used for improving CC transformation and gene targetting in transgenic plants. The RAD51 cnucleotide may be used as probes or amplification primers for detecting, CC quantifying or isolating gene transcripts, in detecting deficiencies in CC the mRNA level during screening for desired transgenic plants, for CC thanges in enzyme activity, for detecting upregulation of expression or CC cranges in enzyme activity, for detecting any number of allelic variants, CC orthologues or paralogues of the gene, or for site directed mutagenesis in enwaryotic cells. It may also be used for recombinant expression of CC its encoded polypeptide, or for use as immunogen in preparing and/or CC screening of antibodies, and in sense or antisense suppression of one or more genes in a host cell, tissue or plant. The RAD51 proteins may be used in assays to agonise or antagonise the enzyme function, or as CC immunogens or antigens to obtain antibodies.

Sequence 1474 BP; 415 A; 337 C; 369 G; 353 T; 0 other;

100.0%;

Score 1474; Pred. No. 0;

DΒ 22;

Length 1474;

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RESULT AAD02120

AAD02120 standard; cDNA; ΒP

28-MAR-2001 (first entry!

Maize orthologue #3 cDNA

orthologue; RAD52 epistasis group; double strand

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is a maize RAD51 orthologue #3 cDNA. RAD51 is one of the genes of the RAD52 epistasis group that is involved in double strand breaks (DSBs) repair by homologous recombination. Control of homologous recombination by modulating RAD51 is used for improving transformation and gene targetting in transformation.
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                                                                                         adenocarcinoma and leukaemia; immune disorders such as AIDS, Addison's disease, diabetes mellitus, rheumatoid arthritis, multiple sclerosis, systemic lupus erythematosus, and myasthenia gravis; infections and trauma. Antagonists of the HTRM polypeptides are useful for treating or preventing disorders associated with increased expression or activity of HTRMs. HTRM polypeptides, their immunogenic fragments or oligopeptides are useful for screening libraries of compounds in drug screening techniques. Polynucleotides encoding HTRM are useful for blocking the transcription of mRNA and regulating gene function by modulating the activity of HTRM vertors expressing under the force of the production of mRNA and regulating gene function by modulating the activity of HTRM vertors expressing under the force of the production of mRNA and regulating gene function by modulating the activity of HTRM vertors expressing under the production of mRNA and regulating the activity of HTRM are useful for blocking the activity of the activity 
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07-AUG-1998;
02-OCT-1998;
                activity of HTRM. Vectors expressing HTRM or agonists can also be us prevent or treat disorder associated with decreased HTRM expression. Antibodies which specifically bind HTRM and polynucleotides encoding
                                                                                                                                                                                                                                                                                                                             nucleotide sequences. The HTRM protein and nucleotide sequences are useful for preventing or treating disorders associated with decreased expression or activity of HTRM which include cell proliferative disorders such as arteriosclerosis and cirrhosis; cancers including
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ52410-Z52474 are human transcriptional regulator molecule
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1325 BP; 399 A; 251
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AAF58252/ ID AAF5 XX

AAF58252 standard; DNA;

936 BP

RESULT

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AAF58252;

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17-MAR-2000;
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                                                                                                                                  936 BP; 4 A; 139 C; 10 G; 7 T; 776 other;
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2000US-0190259.
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No. 1e-13;
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                  The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping, monitoring gene expression.
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17-MAR-2000;
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Sequence 936
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Query Match

6.1%;

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В 22;

Length 936;

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RESULT 7
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DT 24-APR
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                          Synthetic
                                         gene expression;
                                                  Electron-transfer group; ETM; mismatch; genotyping;
                                                                    Oligonucleotide D1954.
                                                                                     24-APR-2001
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1266 agtgaggtgagactggagaatagtaccattttgttgattctcagttgctttgtgccgttg
                                                                                                                                                                                                                            Sequence 936 BP; 5 A; 142 C; 7 G; 6 T; 776 other;
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17-MAR-2000;
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                                                                                                                                                                                               Sequence 936 BP; 6 A; 138 C; 8 G; 8 T; 776 other;
                                                                                                                                                                                                                       monitoring gene expression.
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                                                                                                                                                                                                                                                                                                                                   hybridization assays, e.g. for genotyping, a single surface
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0145695.
2000US-0190259.
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                                                                                                                                                            Score 90.2;
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                                                                                                                                      Mismatches
                                                                                                                                                No.
                                                                                                                                                .2; DB 22;
1e-13;
                                                                                                                                      302;
                                                                                                                                                           Length 936;
                                                                                                                                      Indels
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RESULT 9
AAF58262/c
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Synthetic.
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                                                           26-JUL-1999; 99US-0145695.
17-MAR-2000; 2000US-0190259.
                                                                                       26-JUL-2000; 2000WO-US20476
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                                                                                                                                                                      Electron-transfer group;
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                                                                                                                                                                                                                             AAF58262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1206 tcaagcacttgtatgtccactacgctcctgcagctttcttcgccatggatctttttggact 1265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  490
                                         (CLIN-) CLINICAL MICRO SENSORS
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                                                                                                                                                                                                                                                                                           agtgaggtgagactggagaatagtaccattttgttgattctcagttgctttgtgccgttg 1325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gctaccaaccaaccttaagagagaagtaaatacaacagaacaggctaatatagtgttttg 1385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tcttgataagtctccttcacttccagtagcctcagcaccgtatgcagtgacaggcaaagg 1145
                         RM;
                                                                                                                                                                                                                                                                                                                                                                 gattagagatgctgtgagctcaaaccacaagcgagcccgagtaacgtagcattcttggtg 1205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  atcattgaagttaatgaagattgcaaagacatataacttggcagttgtcttgttgaacca 965
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     monitoring gene expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
                                                                                                                                                                                                                                                                                                                                                                                                          550
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les 8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single-nucleotide polymorphisms, e.g. for genotyping,
                       aaaaaaaaaaaaaaaaaaaaaaaa 1474
                                                                                                                                                                                                                          tcaagcacttgtatgtccactacgctcctgcagctttcttcgccatggatcttttggact 1265
                                                                                                                                                                                                                                                                         gattagagatgctgtgagctcaaaccacaagcgagcccgagtaacgtagcattcttggtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         atcattgaagttaatgaagattgcaaagacatataacttggcagttgtcttgtttgaacca
agtgaggtgagactggagaatagtaccattttgttgattctcagttgctttgtgccgttg
                                                                                                                                                                                                  tcttgataagtctccttcacttccagtagcctcagcaccgtatgcagtgacaggcaaagg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               936 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 A; 139 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              302;
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RESULT 10
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XX Blectr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 938 BP; 4 A; 144 C; 9 G; 5 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     monitoring gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a composition comprising
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-JUL-1999;
17-MAR-2000;
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                                                                                                                                                                                                                                             atcattgaagttaatgaagattgcaaagacatataacttggcagttgtcttgttgaacca
ggcggatatctattacttccggatatgcagttacaccgaacaaattgcagtcataaacta 785
                                                                                                                                                       agtcactactacatttacagaagggtcatttcaattgactcttgctctaggtgacagctg
                                                                                                                                                                                                                                                                                                                           tttccactttcgacaagattttgaagatctggcactgaggaccagagtgctaagtggatt 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        catggagaagttcctcagagagcataaagatgtgcgtatagttattattgatagtgttac 845
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2000US-0190259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 90.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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RESULT 1
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                     The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1086 tettgataagteteetteaetteeagtageeteageaeegtatgeagtgaeaggeaaagg 1145
                                                                                                                                                                                WPI;
                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                gene expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligonucleotide D1835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAF58252 standard;
          monitoring gene expression
                                                                                                   Example 6; Page 127; 159pp; English
                                                                                                                                    Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
                                                                                                                                                                                                                                                          26-JUL-1999; 99US-0145695
17-MAR-2000; 2000US-0190259
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                                                                                                                                                                                                                                                                                                                                                                                                               Electron-transfer group; ETM; mismatch; genotyping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-APR-2001
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                                                                                                                                                                                                                                 (CLIN-) CLINICAL MICRO SENSORS
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              Electron-transfer group;
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No. 1.3e-13;
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                genotyping;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JUL-2000; 2000WO-US20476
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hybridization assays, e.g. for genotyping, allowing repeat analyses
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758 acaccgaacaattgcagtcataaactacatggagaagttcctcagagagcataaagatg 817
                                                                                                        Match 6.1%;
Local Similarity 0.9%;
                                      caacagaacaggctaatatagtgttttgtatctgaacatctggcccatcgtacattcagt 1417
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                                                                                             Conservative 454;
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                                                                                                         Score 89.8; DB Pred. No. 1.3e-13
                                                                                              Mismatches
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RESULT 14
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                                                      26-JUL-2000; 2000WO-US20476
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                                                                                                                                  gene expression; ss
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Best Local Similarity 0.9%;
Matches 7; Conservative 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface
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17-MAR-2000; 2000US-0190259.
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Search completed: October 2, 2001, 05:51:15 Job time: 3021 sec

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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Comp
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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US-08-964-4-8
US-08-969-644-8
US-08-444-189-8
US-08-444-189-8
US-08-261-110A-4
US-08-261-110A-4
US-08-261-110A-4
US-08-261-110A-2
US-08-968-968-12A-109
US-08-968-968-12A-109
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		Sequence 16, Appl	Sequence 6, Appli	Sequence 6, Appli	Sequence 6, Appli	6	Sequence 3, Appli	Sequence 82, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 11, Appl	Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	`	Sequence 3, Appli	Sequence 1, Appli	

## GENERAL INFORMATION: APPLICANT: Havre, Pamela A. APPLICANT: RICE, Michael C. APPLICANT: Holloman, William K. APPLICANT: KMiec, Eric B. TITLE OF INVENTION: REC2 Kinase FILE REFERENCE: 7991-034-999 CURRENT APPLICATION NUMBER: US/09/157,603 CURRENT FILING DATE: 1998-09-21 NUMBER OF SEQ ID NOS: 8 SOCTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 1 LENGTH: 350 TYPE: PRT QΥ 뫄 Qy δÃ В 밁 В ; ORGANISM: Homo Sapiens US-09-157-603-1 Matches Sequence 1, Application US/09157603 Patent No. 6174694 Query Match Best Local : 297 237 198 135 188 VLQRIESLEEEII------SKGIKLVILDSVASVVRKEFDAQLQGNLKERNKFLA 143 YYFRICSYTEQIAVINYMEKFLREHKDVRIVIIDSVTFHFRQDFE-----DLALRTRVLS 197 Local Similarity 32.28; ses 92; Conservation 87 75 27 GDSWSHSCTNRLILHWNGNERYAHL-DKSPSLPVASAPYAVTGKGI 280 GGKAVYIDTEGSFMVERVYQIAEGCIRDILEHFP---HSHEKSSSVQKQLQPERFL-ADI 142 SDELSQXHITTGSGDLNDILGGGIHCKEVTEIGGVPGVGKTQLGIQLAINVQIPVECGGL 86 GNTWSHSVNTRLILQYLDSERRQILIAKSPLAPFTSFVYTIKEEGL 342 REASSLKYLAEEFSIPVILTNQITTHLSGALASQADLYSPADDLSLSEGTSGSSCVIAAL GLSLKLMKIAKTYNLAVVLLNQVTTKF------TEGSFQLTLAL 235 SADFSPAFLSTTLSALDEALHGGVACGSLTEITGPPGCGKTQFCIMMSILATLPTNMGGL 134 EGAVVYIDTESAFSAERLVEIAE-----SRFPRYFNTEEKLLLTSSKVHLYRELTCDE 187 ; Score 323; DB 4; Length 350; ; Pred. No. 1.6e-29; 44; Mismatches 100; Indels 50;

Gaps

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Sequence

RESULT 2 US-09-587-436-1

Sequence 1, Application US/09587436

Patent No. 6210916 GENERAL INFORMATION

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APPLICANT: RICe, Michael C.
APPLICANT: Holloman, William K.
APPLICANT: Kmiec, Eric B.
TITLE OF INVENTION: REC2 Kinase
FILE REFERENCE: 7991-034-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/587,436
CURRENT FILING DATE: 2000-06-05
PRIOR APPLICATION NUMBER: 09/157,603
PRIOR APPLICATION NUMBER: 1998-09-21
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.
                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/157,603
CURRENT FILING DATE: 1998-09-21
RUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo Sapiens
                                                                                                                       ORGANISM: Mus Musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135 EGAVVYIDTESAFSAERLVEIAE-----SRFPRYFNTEEKLLLTSSKVHLYRELTCDE 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 236 GDSWSHSCTNRLILHWNGNERYAHL-DKSPSLPVASAPYAVTGKGI 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 237 REASSLKYLAEEFSIPVILTNQITTHLSGALASQADLVSPADDLSLSEGTSGSSCVIAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             188 VLQRIESLEEEII------SKGIKLVILDSVASVVRKEFDAQLQGNLKERNKFLA
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20 QNAWDM---FSDELSQKHITTGSGDLNDILGGGIHCKEVTEIGGVPGVGKTQLGIQLAIN 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27 SDELSQKHITTGSGDLNDILGGGIHCKEVTEIGGVPGVGKTQLGIQLAINVQIPVECGGL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLSLKLMKIAKTYNLAVVLLNQVTTKF------TEGSFQLTLAL
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                                100;
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Holloman, William K.
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                              Conservative
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7991-034-999
                           20.5%; Score 313; DB 4; L
32.1%; Pred. No. 2.4e-28;
32.1%; Mismatches 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21.1%; Score 323; DB 4; Length 350; 32.2%; Pred. No. 1.6e-29;
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                                                           DB 4; Length 350;
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                              Indels 68;
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SEQ ID NO 3
LENGTH: 350
TYPE: PRT
ORGANISM: Mus Musculus
US-09-587-436-3
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Best Local Similarity
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APPLICANT:
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TITLE OF INVENTION:
FILE REFERENCE: 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
                                281
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GIRDAVSSNHKR 290
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В
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                                                                                                            PKLQGNIKERNKFLGKGASL-LKYLAGEFSIPVILTNQITTHLSGALPSQADLVSPADDL
                                                                                                                                                                  -----DLALRTRVL-SGLSLKLMKIAKTYNLAVVLLNQVTTKF-----------
                                                                                                                                                                                                                              HLCRELTCEGLLQ-----RLESLEEEII---
                                                                                                                                                                                                                                                                                                                                          ATLPTSLGGLEGAVVYIDTESAFTAERLVEIAE-----SRFPQYFNTEEKLLLTSSRV 177
                                                                                                                                                                                                                                                                                                                                                                           VQIPVECGGLGGKAVYIDTEGSFMVERVYQIAEGCIRDILEHFP---HSHEK----SSSV 129
                                                ----TEGSFQLTLALGDSWSHSCTNRLILHWNGNERYAHL-DKSPSLPVASAPYAVTGK 278
                                                                                                                                                                                                                              ----SKGVKLVIVDSIASVVRKEFD
                                                                                                               280
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Sequence 3, Application US/09587436 Patent No. 6210916 CURRENT APPLICATION NUMBER: US/09/587,436 CURRENT FILING DATE: 2000-06-05 FastSEQ for Windows Version RIce, Michael C. Holloman, William K. Havre, Pamela A. N: REC2 Kinase 7991-034-999 1998-09-21 09/157,603

20 QNAWDM----FSDELSQKHITTGSGDLNDILGGGIHCKEVTEIGGVPGVGKTQLGIQLAIN 76 SLSEGTSGSSCLVAALGNTWGHCVNTRLILQYLDSERRQILIAKSPLAAFTSFVYTIKGE 340 PKLQGNIKERNKFLGKGASL-LKYLAGEFSIPVILTNQITTHLSGALPSQADLVSPADDL 280 HLCRELTCEGLLQ-----RLESLEEEII-----SKGVKLVIVDSIASVVRKEFD Q--KQLQPERFLADIYYFRICSYTEQIAVINYMEKFLREHKDVRIVIIDSVTFHFRQDFE 187 ATLPTSLGGLEGAVVYIDTESAFTAERLVEIAE-----SRFPQYFNTEEKLLLTSSRV 177 VQIPVECGGLGGKAVYIDTEGSFMVERVYQIAEGCIRDILEHFP---HSHEK----SSSV 129 QTAYELKTRRSAHLSPAFLSTTLCALDEALHGGVPCGSLTEITGPPGCGKTQFCIMMSVL 124 ----TEGSFQLTLALGDSWSHSCTNRLILHWNGNERYAHL-DKSPSLPVASAPYAVTGK 278 ----DLALRTRVL-SGLSLKLMKTAKTYNLAVVLLNQVTTKF----20.5%; Score 313; DB 4; Length 350 32.1%; Pred. No. 2.4e-28; 46; Mismatches 98; Indels 68; Gaps 224 221 13;

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341 GL---VLQGHER 349

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315 YDSPCLPEAEAMFAINADGVGDA 337

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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 854-3660
TELEFAX: (415) 854-3694
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                  261 DKSPSLPVASAPYAVTGKGIRDA 283
                                                                                                                                                                             150
                                                                                                                                                                                                                     162 TEGTFRPERLLAVAERYGLSG--SDVLDNVAYARAFNTDHQTQLL-------
                                                                                                                                                                                                                                                                                               102 ITTGSKELDKLLQGGIETGSITEMFGEFRTGKTQICHTLAVTCQLPIDRGGGEGKAMYID 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8535-013-999
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                                                                                                                                                                                                                                                                                                                                      35
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                                                                                                                                                                                                                                                          95 TEGSFMVERVYQIAE-----GCIRDILEHFPHSHEKSSSVQKQLQPERFLADIYYFRICS 149
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                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                             AKTYNLAVVLLNQVTTKFTEGSFQLTL----ALGDSWSHSCTNRLILH-WNGNERYAHL 260
                                                                                                                                                                             YTEQIAVINYMEKFLREHKDVRIVIIDSVTFHFRQDFE---DLALRTRVLSGLSLKLMKI 206
                                                                                                                                                                                                                                                                                                                      TTTGSGDLNDILGGGIHCKEVTEIGGVPGVGKTQLGIQLAINVQIPVECGGLGGKAVYID 94
                                                         ADEFGVAVVITNOVVAQ-VDGAAMFAADPKKPIGGNIIAHASTTRLYLRKGRGETRICKI 314
                                                                                                                                      ······YQASAMMVESRYALLIVDSATALYRTDYSGRGELSARQMHLARFLRMLLRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               339 amino acids
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PROTEIN AND DISRUPTION OF PROTEINS THAT ASSOCIATE WITH MAMMALIAN RAd51 FOR HINDERING CELL PROLIFERATION AND/OR VIABILITY OF PROLIFERATING CELLS
                                                                                                                                                                                                                                                                                                                                                                       18.4%; Score 281.5; DB 3 30.4%; Pred. No. 1.2e-24; tive 46; Mismatches 96
                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3; Length 339;
                                                                                                                                                                                                                                                                                                                                                                              96;
                                                                                                                                                                                                                                                                                                                                                                              Indels 41;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
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APPLICATION NUMBER: US/08/964,614A
FILING DATE: 05-NOV-1997
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 650-493-4935
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NAME: Coruzzi, Laura A
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                         102 ITTGSKELDKLLQGGIETGSITEMFGEFRTGKTQICHTLAVTCQLPIDRGGGEGKAMYID 161
315 YDSPCLPEAEAMFAINADGVGDA 337
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                                    261 DKSPSLPVASAPYAVTGKGIRDA 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 0 FILING DATE: 05-NOV-1996
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                                                                                                                                                                                                                                                   95 TEGSFMVERVYQIAE-----GCIRDILEHFPHSHEKSSSVQKQLQPERFLADIYYFRICS 149
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                                                                                                                                                                                                                                                                                                                           35 ITTGSGDLNDILGGGIHCKEVTEIGGVPGVGKTQLGIQLAINVQIPVECGGLGGKAVYID 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE:
                                                                                                      AKTYNLAVVLLNQVTTKFTEGSFQLTL-----ALGDSWSHSCTNRLILH-WNGNERYAHL 260
                                                                                                                                                                                                                  TEGTFRPERLLAVAERYGLSG--SDVLDNVAYARAFNTDHQTQLL------
                                                                    ADEFGVAVVITNOVVAO-VDGAAMFAADPKKPIGGNIIAHASTTRLYLRKGRGETRICKI 314
                                                                                                                                                                                                                                                                                                                                                               80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                            -YQASAMMVESRYALLIVDSATALYRTDYSGRGELSARQMHLARFLRMLLRL 255
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                                                                                                                                                                                                                                                                                                                                                                                18.4%; Score 281.5; DB 3 30.4%; Pred. No. 1.2e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  us 08/758,280
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                                                                                                                                                                                                                                                                                                                                                                                                 DB 3;
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US-08-758-280-1
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US-08-758-280-1
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Patent No. 6037125
GENERAL INFORMATION:
APPLICANT: Hasty, Paul
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LENGTH: 339 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8535-013-999
TELECOMMUNICATION INFORMATION:
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HYPOTHETICAL: NO
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NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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315 YDSPCLPEAEAMFAINADGVGDA 337
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                                    261 DKSPSLPVASAPYAVTGKGIRDA 283
                                                                                                                                                         205
                                                                                                                                                                                                                                                                                                       102 ITTGSKELDKLLQGGIETGSITEMFGEFRTGKTQICHTLAVTCQLPIDRGGGEGKAMYID 161
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                                                                                                                                                                                        150 YTEQIAVINYMEKFLREHKDVRIVIIDSVTFHFRQDFE---DLALRTRVLSGLSLKLMKI 206
                                                                                                                                                                                                                              162 TEGTFRPERLLAVAERYGLSG--SDVLDNVAYARGFNTDHQTQLL------
                                                                                                                                                                                                                                                                95 TEGSFMVERVYQIAE-----GCIRDILEHFPHSHEKSSSVQKQLQPERFLADIYYFRICS 149
                                                                                                                                                                                                                                                                                                                                             35 ITTGSGDLNDILGGGIHCKEVTEIGGVPGVGKTQLGIQLAINVQIPVECGGLGGKAVYID 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                        Match 18.3%; Score 280.5; DB 3 Local Similarity 30.4%; Pred. No. 1.5e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/758,280 FILING DATE: concurrently herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: PENNIE & PROPERTIES STREET: 1155 Avenue of the Americas
                                                                        ADEFGVAVVITNQVVAQ-VDGAAMFAADPKKPIGGNIIAHASTTRLYLRKGRGETRICKI 314
                                                                                                             AKTYNLAVVLLNQVTTKFTEGSFQLTL-----ALGDSWSHSCTNRLILH-WNGNERYAHL 260
                                                                                                                                                                                                                                                                                                                                                                                          80;
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10036-2711
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PROTEIN AND DISRUPTION OF PROTEINS THAT ASSOCIATE WITH
MAMMALIAN RAd51 FOR HINDERING CELL PROLIFERATION AND/OR
VIABILITY OF PROLIFERATING CELLS
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/964,614A
FILING DATE: 05-NOV-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/758,280
FILING DATE: 05-NOV-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Hasty, Paul
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COMPUTER READABLE FORM:
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                                                                                                                   207
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                                261 DKSPSLPVASAPYAVTGKGIRDA 283
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                                                                                                                                                                                                                                                                         95 TEGSFMVERVYQIAE-----GCIRDILEHFPHSHEKSSSVQKQLQPERFLADIYYFRICS 149
                                                                                                                                                                                                                                                                                                                                                 35 ITTGSGDLNDILGGGIHCKEVTEIGGVPGVGKTQLGIQLAINVQIPVECGGLGGKAVYID 94
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OPERATING SYSTEM:
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YDSPCLPEAEAMFAINADGVGDA 337
                                                                        ADEFGVAVVITNQVVAQ-VDGAAMFAADPKKPIGGNIIAHASTTRLYLRKGRGETRICKI 314
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Patent No. 5780296
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APPLICANT: Holloman,
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                   215 DVLSLGRQRHVFSSGSRELDDLLGGGVRSAVLTELVGESGSGKTQMAIQVCTYAALGLVP 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                            393 ALANLHI--AC----VADVEALEHALKYSLPGLIRRLWSSKROSGVSREIGVVVVDNLP 445
                                                                                                                                                                                                                                                                                            275 LSQADDHDKGNNTFQSRTFVRDPIHASTKDDTLSDILQSYGMEPSIGSHRGMG--ACYIT 332
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REGISTRATION NUMBER: 29,
REFERENCE/DOCKET NUMBER:
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                                                                     446 ALFQQDQAAASDIDSLFQRSKMLVEIADALKRISAVQWRGASDCGSSAGRAVLVLNHVSD 505
                                                                                                        180 FHFRQ-----DFEDLALRTRVLSGLSLKLMKIA-----KTYNLAVVLLNQVTT 222
                                                                                                                                                                                 138 FLADIYYFRICSYTEQIAVINYMEKFLR----
                                                                                                                                                                                                                                                                                                                                                                                                                                       y Match 8.2%; Score 126; DB 1;
Local Similarity 20.5%; Pred. No. 9.4e-06;
hes 62; Conservative 52; Mismatches 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
                                   223 KF 224
                                                                                                                                                                                                                                                                                                                                77 ------GLGGKAVYID 94
                                                                                                                                                                                                                                                                                                                                                                                                         28 DELS---QKHI-TTGSGDLNDILGGGIHCKEVTEIGGVPGVGKTQLGIQLAIN----- 76
506 AF 507
                                                                                                                                                                                                                                                         95 TEGS----FMVERVYQIAEGCIRDILEH-FPHSHEKSSSVQ------KQLQPER 137
                                                                                                                                                                                                                     SGGERAAHSIVNRALELASFAINERFDRVYPVCDPTQSSQDADGRRDALLAKAQQLGRRQ 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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COMPOSITIONS AND METHODS TO PROMOTE .
HOMOLOGOUS RECOMBINATION IN EUKARYOTIC CELLS AND ORGANISMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29,258
                                                                                                                                                                                                                                                                                                                                                                                                                                                  52; Mismatches 74; Indels 114; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7991-007
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RESULT 10

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US-09-114-637-2
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Best Local 9
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: COMPOSITIONS AND METHODS TO PROMOTE
TITLE OF INVENTION: HOMOLOGOUS RECOMBINATION IN EUKARYOTIC CELLS AND ORGANISMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: January 17, 1995
ATTORNBY/AGENT INFORMATION:
NAME: Friebel, Thomas E
REGISTRATION NUMBER: 29,258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                               215 DYLSLGRORHVFSSGSRELDDLLGGGVRSAVLTELVGESGSGKTOMAIQVCTYAALGLVP 274
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                                                                                                                                                                                                           138 FLADIYYFRICSYTEQIAVINYMEKFLR-------EHKDVRIVIIDSVT 179
                                                                                                                                                                                                                                                       333 SGGERAAHSIVNRALELASFAINERFDRVYPVCDPTQSSQDADGRRDALLAKAQQLGRRQ 392
                                                                                                                                                                                                                                                                                                                                          275 LSQADDHDKGNNTFQSRTFVRDPIHASTKDDTLSDILQSYGMEPSIGSHRGMG--ACYIT 332
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                                                                              446 ALFQQDQAAASDIDSLFQRSKMLVEIADALKRISAVQWRGASDCGSSAGRAVLVLNHVSD 505
                                                                                                                        180 FHFRQ------DFEDLALRTRVLSGLSLKLMKIA------KTYNLAVVLLNQVTT 222
                                                                                                                                                                    393 ALANLHI--AC----VADVEALEHALKYSLPGLIRRLWSSKRQSGVSREIGVVVVDNLP 445
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506 AF 507
                                       223 KF 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28 DELS---OKHI-TTGSGDLNDILGGGIHCKEVTEIGGVPGVGKTQLGIQLAIN----- 76
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                                                                                                                                                                                                                                                                                                95 TEGS----FMVERVYQIAEGCIRDILEH-FPHSHEKSSSVQ------KQLQPER 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 8.2%; Score 126; DB 2; Length 781; Local Similarity 20.5%; Pred. No. 9.4e-06; es 62; Conservative 52; Mismatches 74; Indels 1:
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                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                           310 QYKLNLIANQIRLLRKEDRVDVIFIDYLQLINSSVGENRQNEIADI---SRTLRGLASEL 366
                                                               152 E-QIAVINYMEKFLREHKDVRIVIID------SVTFHFRQDFEDLALRTRVLSGLSLKL 203
                                                                                                   255 -LEMSAGQIVERIIANLTGISGEKLQRGDLSKEELFRVEEAGETVR----ESHFYICSDS 309
                                                                                                                                                                            203 TGYKDIDDKGVILAKG----NEVIIAARPSIGKTALAIDMAINLAVTQQRRVGFLS---- 254
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ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
204 MKIAKTYNLAVVLLNQVTTK 223
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CURRENT APPLICATION DATA:
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                                                                                                                                        92 YIDTEGSFMVERVYQIAEGCIRDILEHFPHSHEKSSSVQKQLQPERFLADIYYFRICSYT 151
                                                                                                                                                                                                               37 TGSGDLND---ILGGGIHCKEVTEIGGVPGVGKTQLGIQLAINVQIPVE--CGGLGGKAV 91
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                                                                                                                                                                                                                                                                                       Local
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                                                                                                                                                                                                                                                                     51;
                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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                                                                                                                                                                                                                                                                             7.0%; Score 107; DB 3; 25.5%; Pred. No. 0.00067;
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                                                                                                                                                                                                                                                               39;
                                                                                                                                                                                                                                                             Mismatches
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
152 E-QIAVINYMEKFLREHKDVRIVIID------SVTFHFRQDFEDLALRTRVLSGLSLKL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION: NAME: Svensson, Leonard
                                                  255 -LEMSAGQIVERIIANLTGISGEKLQRGDLSKEELFRVEEAGETVR----ESHFYICSDS 309
                                                                                                                        203 TGYKDIDDKGVILAKG----NFVIIAARPSIGKTALAIDMAINLAVTQQRRVGFLS---- 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                    92 YIDTEGSFMVERVYQIAEGCIRDILEHFPHSHEKSSSVQKQLQPERFLADIYYFRICSYT 151
                                                                                                                                                          37 TGSGDLND---ILGGGTHCKEVTETGGVPGVGKTQLGTQLAINVQIPVE--CGGLGGKAV 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Svensson, Leonard R. REGISTRATION NUMBER: 30,33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          367 -----NIPIVCLSQLSRK 379
                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/07/991,512 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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                                                                                                                                                                                                                  Score 107; DB 3; Length 451; Pred. No. 0.00067;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,544
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 12
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 07-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Giuliani, Marzia M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           367
             152 E-QIAVINYMEKFLREHKDVRIVIID-----SVTFHFRQDFEDLALRTRVLSGLSLKL
                                                     255 -LEMSAGQIVERIIANLTGISGEKLQRGDLSKEELFRVEEAGETVR----ESHFYICSDS
                                                                                                                         203
                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 703-241-2848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: IT M. FTI.ING DATE: 07-FEB-1991
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                                                                                     92 YIDTEGSFMVERVYQIAEGCIRDILEHFPHSHEKSSSVQKQLQPERFLADIYYFRICSYT 151
                                                                                                                                                                                                                                                                                                                                                 TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER:
                                                                                                                                                              37 TGSGDLND---ILGGGIHCKEVTEIGGVPGVGKTQLGIQLAINVQIPVE--CGGLGGKAV 91
                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 30,330
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                                                                                                                         TGYKDIDDKGVILAKG----NFVIIAARPSIGKTALAIDMAINLAVTQQRRVGFLS---- 254
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TRACHOMATIS SEROTYPE D, ITS GENES AND PROTEINS ENCODED BY
THEM; RECOMBINANT PLASMIDS FOR THE EXPRESSION OF SAID
GENES IN HETEROLOGOUS SYSTEMS, PREPARATION OF SAID
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Pred. No. 0.00067;

rematches 74; Indels 36;
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US-08-446-920-2
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTTWARE: PatentIn Rclease #1.0, CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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                                  197
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 173
                                                                  114 NLLVSQPSTGEEALEILETITRS-GGIDLVVVDSVAALTPKAEIDGDMGDQHVGLQARLM
                                                                                                    153 QIAV-----INYMEKFLREHKDVRIVIIDSVT----FHFRODFED--LALRTRVL 196
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TELEFAX: 404/688-9880
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                                                                                                                                                                        94 DTEGSFMVERVYQIAEGCIRDILEHFPHSHEKSSSVQKQLQPERFLADIYYF-RICSYTE 152
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                                 SGLSLKLMKIAKTYNLAVVLLNQVTTK 223
                                                                                                                                         DAEHAL ---
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SHALRKITGVLHKMNTTLIFINQIRMK 199
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Y: USA
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                                                                                                                                                                                                                                                                                                                                                                                                        linear
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22.7%;
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                                                                                                                                                                                                                                                                                 Mismatches
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; Sequence 2, Application US/08446920

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; TELEPHONE: 404/688-0770
; TELEFAX: 404/688-980
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-446-920-2
Search completed: October 1, 2001, 16:27:48 Job time: 21 sec
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GENERAL INFORMATION:
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NAME: Spratt, Gwendolyn D.
REGISTRATION NUMBER: 36,016
REFERENCE/DOCKET NUMBER: 2200.037
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404/688-0770
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION PATE:
CURRENT APPLICATION NUMBER: US/08/446,920
APPLICATION NUMBER: US/08/446,920
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APPLICANT: Blaser, Martin J.
TITLE OF INVENTION: RECOMBINASE-DEFICIENT HELICOBACTER
TITLE OF INVENTION: PYLORI AND RELATED METHODS
NUMBER OF SEQUENCES: 11
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                                                                                                                        173 SHALRKITGVLHKMNTTLIFINQIRMK 199
                                                                                                                                                                         197 SGLSLKLMKIAKTYNLAVVLLNQVTTK 223
                                                                                                                                                                                                                       114 NLLVSQPSTGEEALEILETITRS-GGIDLVVVDSVAALTPKAEIDGDMGDQHVGLQARLM 172
                                                                                                                                                                                                                                                                        153 QIAV-----INYMEKFLREHKDVRIVIIDSVT----FHFRQDFED--LALRTRVL 196
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CITY: Atlanta
STATE: Georgia
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ZIP: 30303
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Sorghum propinquum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 596)
                                                                                                                                                                                                   BG051275 596 bp mRNA EST 25-JAN-20 FM1_54_D07.91_A003 Floral-Induced Meristem 1 (FM1) Sorghum propinguum cDNA, mRNA sequence.
BG051275
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EST.
                                  Cordonnier-Pratt, M.-M.,
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                                    Gingle, A., Sudman, M., Marsala, C.
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AV629583 AV629583
AA641847 ms19903r
BG131647 EST464539
BG405188 602418623
BF240472 601875867
AL533302 AL533302
BG521224 ps44c04.y
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AL530472 AL530472
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AZ687391 ENTJB81TF
AL533348 AL533348
AZ677092 ENTKU28TR
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AA702444 zi89b09.s
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Contact: Cordonnier-Pratt MM
Department of Botany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: PolyTMix
High quality sequence start:
High quality sequence stop:
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Sequences have been trimmed
below Phred quality 16. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 706 542 1860
Fax: 706 542 1805
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/note="Organ: Floral-induced meristems; vector:
/note="Organ: Floral-induced meristems; vector:
pBluescript II from Lambda Zap II; Site_1: XhOI; Site_2:
ECORI; mature plants were placed in a growth chamber for
15 days with 16 hr darkness and 8 hr light (flowering is
induced by short-day conditions); 16 days after being
returned to the greenhouse under natural long days during
late April/early May, meristems were harvested The
library was made from poly-A RNA in the cloning vector
lambda Zap II. Clones to be sequenced were prepared by
mass excission."

a 132 c 129 g 165 t
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/db_xref="taxon:132711"
/clone_lib="Floral-Induced Meristem 1 (FM1)"
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SOURCE ORGANISM VERSION KEYWORDS

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                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
gctaccaaccaaccttaagagagaagtaaatacaacagaacaggctaatatagtgttttg
                                                        agtgaggtgagactggagaatagtaccattttgttgattctcagttgctttgttgccgttg 1325
                                                                                                                                                                                                                                                                          tcttgataagtctccttcacttccagtagcctcagcaccgtatgcagtgacaggcaaagg
                                                                                                                                                                                                                                                                                                                                                TCAAGCACTTGTATCTCCACTATGCTCTTGCAGCTTTCTTCACCATGGATCTTTGGGGCA
                                                                                                                             | teaageacttgtatgteceactaegetectgeagetttettegeeatggatetttttggaet 1265
                                                                                                                                                                                GATTAGAGATGCTGTGAGTCCAAACCACAAACGAGCCCGAGTAACGTAGCATTCTTGGTG
                                                                                                                                                                                                   gattagagatgctgtgagctcaaaccacaagcgagcccgagtaacgtagcattcttggtg
                                                                                                                                                                                                                                                        CCTTGATAAGTCTCCTTCACTTCCAGTAGCCTCAGCACCGTATGCAGTGACAGGCAAAGG
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1 (bases 1 to 543)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mmpratt@uga.edu
Seq primer: PolyTMix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Department of Botany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               An EST database from Sorghum: Sorghum propinquum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cordonnier-Pratt, M.-M., Gingle, A.,
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nt Sciences Building, Rm.
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/note="Organ: Rhizomes; Vector: pBluescript II from Lambda
Zap II; Site_1: XhOI; Site_2: EcoRI; The library was made
from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."
122 c 119 g 150 t
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/db_xref="taxon:132711"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 382; DB 155;
Pred. No. 1.9e-90;
D; Mismatches 35;
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BG606048
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JOURNAL
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   454
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                ggcagtttcatggttgaacgtgtctaccagattgctgaagggtgtattagggacatactg
                                                                                                                                         ACTGGTGCTGGTGACCTCAATGACATACTTGGTGGCGGGATTCACTGCAAAGAAGTTACT 333
                                                                                                                                                                                                       actggttctggtgacctcaatgacatacttggtggcgggattcactgcaaagaagttact 477
GGAAGTTTCATGGTTGAACGTGTCTACCAGATTGCTGAAGGGTGTATCAGGGACATACTG
                                                             GTACAAATCCCAGTGGAATATGGTGGCCTTGGTGGGAAAGCAGTTTATATCGATACAGAA
                                                                                                                         TATCTGAACATGTGGCACATCTTGCATTCAGTAA 451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mmpratt@uga.edu
Seq primer: JEN REV
High quality sequence '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The University of Georgia
Plant Sciences Building, Rm.
Tel: 706 542 1805
Fax: 706 542 1805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Cordonnier-Pratt Department of Botany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cordonnier-Pratt, M.-M., Gingle, A., Paterson, A., Sudman, M. and Pratt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clade; Panicoideae; Andropogoneae; 1 (bases 1 to 614)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
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                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Sorghum propinguum"
/db_xref="taxon:132711"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Rhizome2 (RHIZ2)"
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95.5%;
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Rhizome2
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Pred. No. 7.7e-88;
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Best Local S
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  164
                                                                                               104 CGCAGAAGCTGCTCCTCCAAGGAGCCCAAAATGCATGGGATATGCTGTCTGAGGAGCAAT 163
                                                                                                                              341 cacaacagaagtacgtttcaggagcccagaatgcctggggatatgttctctgatgagctgt 400
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  CACAGAAACACATCACTACTGGCTCTGGTGACCTGAACGGCATACTTGGTGGAGGGATTC 223
                         cacagaaacacatcactactggttctggtgacctcaatgacatacttggtggcgggattc 460
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Sequence have been trimmed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Olin Anderson
US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 603)
Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han ,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L. and Tong,J.C.
The structure and function of the expressed portion of the wheat genomes - Vernalized crown cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Triticum aestivum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             quality sequence with phred score less than
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldea
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                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                              /lbb_host="E. coll SOLR"
//note="Vector: Lambda Uni-ZAP XR, excised phagemid;
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; Seeds were germinated and
grown at 4 C for 5 weeks. The tissue, total RNA, and
poly(A) RNA were prepared, a cDNA library was made, and
the CDNA clones were in vivo excised to give pBluescript
phagemids in the TJ Close lab (Choi, Close, Fenton) at
the University of California, Riverside, Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE0804_H03_P06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cultivar="Chinese
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                                                                                                                                                                                          Score 367.2; DB 1
Pred. No. 1.6e-86;
0; Mismatches 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
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Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Department of Biological Sciences
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/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site_1: BamHI; Site_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web
                                                                                                                           /cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/clone_lib="1006 - RescueMu Grid G"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
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                                                                                                                                                                                        Stanford University
855 California Ave, I
Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                     Email: walbot@stanford.edu
Possible ligation site of ends cut
Reverse complemented post-ligation
Plate: 1006003 row: H column: 03
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Contact: Walbot V
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                /cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
                                                   /organism="Zea mays"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76
An EST database from Sorghum: f
Unpublished (2000)
Contact: Cordonnier-Pratt MM
Department of Botany
The University of Georgia
Plant Sciences Building, Rm. 25
Tel: 706 542 1860
Fax: 706 542 1805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATCAATCTGGC
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                                                                                                                                                                                                                                                                             Sorghum propinquum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 481)
                                                                                                                                                                                                                                                           Cordonnier-Pratt, M.-M., Gingle, A., Sudman, M., Marsala, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BG050955 481 bp mRNA EST FM1_54_D07.b1_A003 Floral-Induced Meristem
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sorghum propinguum.
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//lab_host="D
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/dev_stage="adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GI:12504184
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9.
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                                                                 Athens, GA 30602-7271, USA
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RESULT 8
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JOURNAL
                                                                                                                                                                                       AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ggcagtttcatggttgaacgtgtctaccagatt 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        actggttctggtgacctcaatgacatacttggtggcgggattcactgcaaagaagttact 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCTGGGGCCCAGAATGCTTGGGATATGCTATCTGATGAGCAGTCACAGAAACACATCACT 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | tcaggagcccagaatgcctgggatatgttctctgatgagctgtcacagaaacacatcact 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGAAGTTTCATGGTTGAACGTGTCTACCAGATT 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTACAAATCCCAGTGGAATATGGTGGCCTTGGTGGGAAAGCAGTTTATATCGATACAGAA 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTGGTGCTGGTGACCTCAATGACATACTTGGTGGCGGGATTCACTGCAAAGAAGTTACT 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AW310460 670 bp mRNA EST 17-JUL-2000 sf36d09.x1 Gm-c1028 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1028-2058 3' similar to TR:022144 022144 PUTATIVE DNA REPAIR
                                      Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C. Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurl, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and Wilson, R.
                      Public Soybean EST Project
                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Glycine.
                                                                                                                                                                                                                                                                                                                   soybean.
Glycine max
                                                                                                                                                                                                                                                                                                                                                                           EST
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                                                                                                                                                                                                                                                                                                                                                                                                 AW310460.1 GI:6726061
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: JEN REV
                                                                                                                                                                                                             (bases 1 to 670)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Organ: Floral-Induced meristems; Vector: pBluescript II from Lambda Zap II; Site_1: XhOI; Site_2: ECORI; mature plants were placed in a growth chamber for 15 days with 16 hr darkness and 8 hr light (flowering is induced by short-day conditions); 16 days after being returned to the greenhouse under natural long days during late April/early May, meristems were harvested The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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/db_xref="taxon:132711"
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95.2%;
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Pred. No. 3.2e-56;
""smatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 173; Length 481;
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                                                                                                                                                     Beck, C.,
                                                                                                                                                                            Khanna
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                                                                 545
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                                                                                                                                                                                                                                                                                                            665
                                                                                                                                                                                                                                                                                                                                     720 tttcctggcggatatctattacttccggatatgcagttacaccgaacaaattgcagtcat 779
900 tggattatcattgaagttaatgaagattgcaaagacatataacttggcagttgtcttgtt 959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                              tgttactttccactttcgacaagattttgaagatctggcactgaggaccagagtgctaag 899
                                                                                                                                                                                                              aaactacatggagaagttcctcagagagcataaagatgtgcgtatagttattattgatag 839
                                                              TGTTACTTTCCACTTCCGCCAAGACTTTGATGATATGGCTCTCAGGACTCGATTACTCAG
                                                                                                                                                                                                                                                                                                         TATCTTAGAAAATATTCTATNTTCGTGTTTGCAGCTACACTGAGCAAATTGCTTTGAT 606
                                                                                                                                                                                     AAATTACTTGGACAAATTCATCACAGAGAATAAAGATGTAAAGATCCTCATTGTTGACAG 546
                                                                                                                                                                                                                                                                                                                                                                                                                                347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 462.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Other_ESTs: sf36d09.yl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4444 Forest Park Parkway, Box 8501,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                218
                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       first-strand synthesis primer was used. An 'anchor' nucleotide (V=A,C, or G) was added to the 3' end of the primer [GAGAGAGAGAGAGAGAGAGAGAGAGTQTCCGAG(T)]8V] to anchor the primer at the 5' end of the poly(A) tract. After second-strand synthesis, the cDNA ends were filled in with cloned pfu DNA polymerase, ligated to EcoRI adapters and subsequently phosphorylated. The XhOI site within the first-strand synthesis primer was then restricted by digestion with XhOI, all XhOI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500bp cutoff, using GibcoBRL Life Technologies' CDNA Size Fractionation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              column. The column eluent was then ligated into Stratagene's pBluescript II XR Predigested vector (pBluescript II SK(+) that has beeingested with EcoRI and XhoI, and phosporylated by Stratagene). Both the white and blue colonies appear to contain recombinant plasmids with cDNA inserts, based on size (n-25). This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             library was constructed by Dr. Paul Keim and Coryell."

117 c 125 g 209 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          japonicus, strain USDA110 priot to harvest. Stratagene's CDNA synthesis Kit (catalog number 200401) was used to synthesize the CDNA. First-strand synthesis was performed with 5-methyl dCTP, hence the ligated cDNA was hemimethylated. A modification of Stratagene's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pBluescript II XR; Site_1: EcoRI; Site_2: XhoI; The mRNA was isolated from roots of Glycine max 'Supernod' plants generously donated by Dr. Gary Stacey. The seedlings were innoculated with Bradyrhizobium
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/tissue_type="roots of 'Supernod' plants"
/lab_host="DH10B"
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/db_xref="taxon:3847"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              caaagggattagagatgctgtgagctcaaaccacaagcgagcccgagtaacgtagcattc 1199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sf36d09.yl Gm-c1028 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1028-2058 5' similar to TR:022144 022144 PUTATIVE DNA REPAIR
                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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1 (bases 1 to 506)
                                                                                                                                                                                                                                                                           High quality sequence stop: 414.
                                                                                                                                                                                                                                                                                                info@genomesystems.com web site: www.genomesystems.com
Insert Length: 1400 Std Error: 0.00
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314 286 1810
/note-"Vector: pBluescript II XR; Site_1: EcoRI; Site_2: XhoI; The mRNA was isolated from roots of Glycine max 'Supernod' plants generously donated by Dr. Gary Stacey. The seedlings were innoculated with Bradyrhizobium
                                                                                      /db_xref="taxon:3847"
/clone="GRNOME SYSTEMS CLONE ID: Gm-c1028-2058"
/clone_lib="Gm-c1028"
/tissue_type="roots of 'Supernod' plants"
/lab_host="DH10B"
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774

115201 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence. AW784884

GI:7841660

AW784884

506 bp

09-JUL-2000

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

Sus scrota

EST AW784884.1 밁 Qγ 밁 δÃ В δõ 밁 Qy 멍 Š 밁

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Query Match
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597 TTTGATAAA 605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   474 tactgagatcggtggcgtcccaggggttggtaaaactcaactggggattcaactagcaat 533
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                                                            agtcataaa 782
                                                                                                                               TTATTATATCTTAGGAAATATATTCTATTTTCGTGTTTGCAGCTACGCTGAGCACATTGC
                                                                                                                                                              tgagcgtttcctggcggatatctattacttccggatatgcagttacaccgaaccaaattgc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cloned Pfu DNA polymerase, ligated to EcoRI adapters and subsequently phosphorylated. The xhoI salte within the first-strand synthesis primer was then restricted by digestion with xhoI; all xhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500bp cutoff, using GlbcoBRI Life Technologies' cDNA Size Fractionation column. The column eluent was then ligated into Stratagene's pBluescript II XR Predigested vector (pBluescript II XR) that has been digested with EcoRI and XhoI, and phosporylated by Stratagene). Both the white and blue colonies appear to contain recombinant plasmids with cDNA inserts, based on size (n=25). This library was constructed by Tr paul Keim and Tr Virding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                library was constructed by Dr. Paul Keim and Coryell."

a 110 c 149 g 167 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 first-strand synthesis primer was used. An 'anchor' nucleotide (V=A,C, or G) was added to the 3' end of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.0%;
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Pred. No. 2.9e-36;
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                                                                                                                                                                                                                                                                                                  381 GTGAAGCAGTTTTTATTGATACAGAGGGGAGTTTTATGGTTGATAGAGTAGTAGACCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                            261 GTGGAGTACCCTTAACCAAAATAACAGAAATTTGTGGTGCACCAGGTGTTGGAAAAAACAC 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USDA,
PO Bos
Tel: '
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 550)
                                                                                                                         mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore
                                               Homo sapiens
                                                                                            BG471853.1 GI:13404128
                                                                                                           BG47185
                                                                                                                                        602513325F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:4635918
                                                                                                                                                         BG471853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BACKWARD: GTTTTCCCAGTCACGACG
Plate: 45 row: L column: 4
Seq primer: ATTTAGGTGACACTATAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and Keele,J.W. Design and use of two pooled tissue normalized cDNA libraries for
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1 91 c 126 g 124 t
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/db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="pooled"
/lab_host="DH10B"
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61.7%;
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                                         tgattctgcactggaatgggaacgaacgatacgcacatcttgataagtctcc 1100
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                                                                                                                                                                                                                                                           CAAATAATCACAGATTAGCTGTAATTTTAACCAATCAGATGACAACAAGATTGATAAGA
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
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/lab_host="DH10B (page-resistant)"
/lab_host="DH10B (page-resistant)"
/note="Organ: eye: Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRT/XhoI sites using the following 5; adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
61 a 109 c 120 g 160 t
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/db_xref="taxon:9606"
/clone="IMAGE:4635918"
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                ggaaagcagtttatatagatacagagggcagtttcatggttgaacgtgtctaccagattg 631
                                                                                          aactggggattcaactagcaatcaatgtacaaatcccagtggaatgtggtggccttggtg 571
                                                                                                                                                                  gcgggattcactgcaaagaagttactgagatcggtggcgtcccaggggttggtaaaactc 511
                                                                                                                                                                                                                     AGGAGCATACCCAGGCTTTCATAATCACTTTCTGTTCAGCACTAGATGATATTCTTGGGG 620
GTGAAGCAGTTTTTATTGATACAGAGGGAAGTTTTATGGTTGATAGAGTGGTAGACCTTG
                                                                         AATTATGTATGCAGTTGGCAGTAGATGTGCAGATACCAGAATGGTTTGGAGGAGTGGCAG
                                                                                                                                                 GTGGAGTGCCCTTAATGAAAACAACAGAAATTTGTGGTGCACCAGGTGTTGGAAAAACAC 560
                                                                                                                                                                                                                                                                                               162;
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Insert Length: 892 Std Error: 0.00
Seq primer: -40UP from Gibco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1997)
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National Cancer Institute, Cancer Genome Anat
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/db_xref="taxon:9606"
/clone="IMAGE:1753094"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Soares_testis_NHT"
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Pred. No. 1.4e-15;
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                                                                                                                                                                                                                                                                                                                                             392 atgagctgtcacagaaacacatcactactggttctggtgacctcaatgacatacttggtg 451
  ctgaagggtgtattagggacatactg 657
                                                GTGAAGCAGTTTTTATTGATACAGAGGGAAGTTTTATGGTTGATAGAGTGGTAGACCTTG
                                                                     ggaaagcagtttatatagatacagagggcagtttcatggttgaacgtgtctaccagattg
                                                                                                                                           AATTATGTATGCAGTTGGCAGTAGATGTGCAGATACCAGAATGTTTTGGAGGAGTGGCAG
                                                                                                                                                                                aactggggattcaactagcaatcaatgtacaaatcccagtggaatgtggtggccttggtg
                                                                                                                                                                                                                              GTGGAGTGCCCTTAATGAAAACAACAGAAATTTGTGGTGCACCAGGTGTTGGAAAAACAC
                                                                                                                                                                                                                                                   gcgggattcactgcaaagaagttactgagatcggtggcgtcccaggggttggtaaaactc 511
                                                                                                                                                                                                                                                                                                                        AGGAGCATACCCAGGGCTTCATAATCACCTTCTGTTCAGCACTAGATGATATTCTTGGGG 281
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1. (bases 1 to 658)
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601283055F1 NIH_MGC_44
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Plate: LLCM252 row: m column: 13
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="Taxon:9606"
/clone="IMAGE:3605172"
/clone=lib="NHMGE:3605172"
/clone=lib="NHH_MGC_44"
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/tab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling
Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
.83 a 134 c 163 g 178 t
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Best Local Similarity 60.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                    263 AGGAGCATACCCAGGGCTTCATAATCACCTTCTGTTCAGCACTAGATGATATTCTTGGGG 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   392 atgagetgteacagaaacacateactactggttetggtgaceteaatgacatacttggtg 451
                                                 632 ctgaagggtgtattagggacatactg 657
  CTACTGCCTGCATTCAGCACCTTCAG
                                                                                                     GTGAAGCAGTTTTTATTGATACAGAGGGAAGTTTTATGGTTGATAGAGTGGTAGACCTTG 502
                                                                                                                                                                                                              AATTATGTATGCAGTTGGCAGTAGATGTGCAGATACCAGAATGTTTTGGAGGAGTGGCAG 442
                                                                                                                                                                                                                                          aactggggattcaactagcaatcaatgtacaaatcccagtggaatgtggtggccttggtg 571
                                                                                                                                                                                                                                                                                                              GTGGAGTGCCCTTAATGAAAACAACAGAAATTTGTGGTGCACCAGGTGTTGGAAAAACAC 382
                                                                                                                                                                                                                                                                                                                                                          gcgggattcactgcaaagaagttactgagatcggtggcgtcccaggggtttggtaaaactc 511
                                                                                                                                                    ggaaagcagtttatatagatacagagggcagtttcatggttgaacgtgtctaccagattg 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM318 row: k column: 06
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NIH-MGC http://mgc.nci.nih.gov/
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/tissue_type="choriocarcinoma"
/tab_host="DBHOB (phage resistant)"
/note="organ: placenta; vector: pOTB7; Site_1: XhoI;
/note="organ: placenta; vector: pOTB7; Site_1: EcoRI; cDNA made by oligo-dT priming: placenta; cDNA made by oligo-dT priming the Directionally cloned into EcoRI/XhoI sites using the pirectionally cloned into EcoRI/XhoI sites using the following 5 adaptor: GGCAGGAG(G), Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-DNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
a 136 c 170 g 182 t
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/db_xref="taxon:9606"
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Pred. No. 3.7e-15;
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539
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                                                                                                                                                                                                                                                            359 GTGGAGTGCCCTTAATGAAAACAACAGAAATTTGTGGTGCACCAGGTGTTGGAAAAAACAC
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                                                                                                                                                                                         aactggggattcaactagcaatcaatgtacaaatcccagtggaatgtggtggccttggtg 571
                                                                                                                                                                                                                                                                                gcgggattcactgcaaagaagttactgagatcggtggcgtcccaggggttggtaaaactc 511
CTACTGCCTGCATTCAGCACCTTCAG 564
                                  ctgaagggtgtattagggacatactg 657
                                                                                    GTGAAGCAGTTTTTATTGATACAGAGGGAAGTTTTATGGTTGATAGAGTGGTAGACCTTG 538
                                                                                                                                                                       AATTATGTATGCAGTTGGCAGTAGATGTGCAGATACCAGAATGTTTTGGAGGAGTGGCAG
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI015 row: h column: 09
High constitution
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1 (bases 1 to 778)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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/db_xref="taxon:9606"
/clone="IMAGE:4419512"
/clone="IMAGE:4419512"
/clone="ibb="NIH_MGC_B5"
/tissue_type="lymphoma, cell line"
/lab_host="DH1DB (phage-resistant)"
/lab_host="Dymph" Vector: pcMv-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.867 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

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SPTREMBL_16:*

1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
4: sp_human:*
5: sp_inverteb:
6: sp_mammal:*
7: sp_mhc:*
8: sp_organel1:
9: sp_plage:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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299	299	299	299.5	302	303.5	309	313	316	318	330.5	345	346	358	395	417	886	1010	1014	Score
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251.5	254	255.5	260.5	262.5	265.5	268.5	269.5	271.5	273.5	273.5	276.5	280	280	280	280	280.5	282.5	283.5	284.5	290	293.5	294.5	296.5	297.5	298
16.4	16.6	16.7	17.0	17.2	17.4	17.5	17.6	17.7	17.9	17.9	18.1	18.3	18.3	18.3	18.3	18.3	18.5	18.5	18.6	19.0	19.2	19.2	19.4	19.4	19.5
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093756 sulfolobus	093758 uncultured	O58001 pyrococcus	Q9uul2 schizosacch	093771 uncultured	P87210 neurospora	093762 uncultured	Q9p956 penicillium	Q9xed6 zea mays (m	P78579 emericella	P78613 emericella	P94102 arabidopsis	Q9u6wl trypanosoma	077135 drosophila	001679 bombyx mori	000847 trypanosoma	093747 halobacteri	074569 coprinus ci	09xed7 zea mays (m	Q9w628 cynops pyrr	061127 leishmania	Q9hmm4 halobacteri		076341 tetrahymena	_	093748 cenarchaeum

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255 DYDDLAQRTRVLSEMALKFMKLAKKFSLAVVLLNQVTTKFSEGSFQLALALGDSWSHSCT 314	185 DFEDLALRTRVLSGLSLKLMKIAKTYNLAVVLLNQVTTKFTEGSFQLTLALGDSWSHSCT 244	195 HFQANQVQMKPEDILENIFYFRVCSYTEQIALVNHLEKFISENKDVKVVIVDSIFFHFRQ 254	꼾	135 GKTQIGIQLSVNVQIPRECGGLGGKAIYIDTEGSFMVERALQIAEACVEDMEEYTGYMHK 194	65 GKTQLGIQLAINVQIPVECGGLGGKAVYIDTEGSFMVERVYQIAEGCIRDILEHFPHSHE 124	80 NGSRSLINGAKNAWDMLHEEESLPRITTSCSDLDNILGGGISCRDVTEIGGVPGI 134	GPQQKYVSGAQNAWDMFSDELSQKHITTGSG	Local Similarity 64.7%; Pred. No. 2.3e-76; nes 187; Conservative 56; Mismatches 40;	Match 66.3%;	SEQUENCE 363 AA; 40214 MW; DC38925F9459F25C CRC64;	EMBI: ATTOGETA, CACTATOR IN EMPLY WELLBALK/DUBS (ACADASES.	TOTAL SECTIONS OF THE CONTRACT OF SECTIONS	STRAIN=CV. COLUMBIA;	SEQUENCE FROM N.A.	[1]	NCBI_TaxID=3702;	Magnorrophyta, edutocryredoms, core edutocs, mostdae, editosids II; Brassicales: Brassicaceae: Arabidonsis.	yophyta; Tracheophyta; Spermatophy	Arabidopsis thaliana (Mouse-ear cress).		DANSIO BOOMBIN	(TrEMBLrel. 16, Last	-2001 (TrEMBLrel.		ETRO DEFIINTMARY.	л 1	

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01-MAR-2001 (TrEMBLrel. 1
RAD51C PROTEIN.
 STRAIN=CV. COLUMBIA; Rounsley S.D., Lin X Sykes S.M., Mason T.
                                                              Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta;
Magnoliophyta; eudicotyledons; core eud
Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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O1-JAN-1998 (TrEMBLrel. 05,
O1-JUN-2000 (TrEMBLrel. 14,
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
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40213 MW; E21D09EC0A79FA7A CRC64;
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R., Adams M.D.,
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PRINTS; PR00142; RECA.
SMART; SM00382; AAA; 1.
SEQUENCE 319 AA; 35320
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Q9YFY1;
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01-NOY-1999 (TrEMBLrel. 12, Created)
01-NOY-1999 (TrEMBLrel. 12, Last sequence update)
01-NOY-1999 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AC002387; AAB82635.1; -.
InterPro; IPR001533; -.
SEQUENCE 332 AA; 36864 MW; A7F058BFD54B8A66 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                      Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Ku Hosoyama A., Fukui S., Nagai Y., Nishijina K., Nakazawa H., Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Nakamura Y., Nomura N., Sako Y., Kikuchi H.; Nomura N., Sako Y., Kikuchi H.; "Complete genome sequence of an aerobic hyper-thermophilic
                                                                                                                                                                                                                                                                                                                                       crenarchaeon, Aeropyrum pernix K1.";
DNA Res. 6:83-101(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99310339; PubMed=10382966;
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                                                                                                                                                                                                                                                                                                                        EMBL;
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OKYVSGA------QNAWDMFSDELSQKHITTGSGDLNDILGGGIHCKEVTEIGGVPGV 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YIDKSPSLPSASASYTVTSRGLRNS-SSSSKRVKM
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                                                                        Score 417; DB 1;
Pred. No. 7.8e-27;
1; Mismatches 86
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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                                                                           SAPYAVTGKGIRDA 283
                                                                                              VAVVVTNQVMARPDVFYGDPTTAVGGHVLAHTPGVRIQLRKSKGNKRIARVVDAPHLPEG
                                                                                                                                 AIVDELFTFVPKN-DVRLVILDSVTSHFRAEYPGREHLAERQQKLNSHLHQLMRLAEAYN
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                                                                                                                                                                                                                                            Score 395; DB 1; Li
Pred. No. 5.4e-25;
Pred. No. 5.4e-25;
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            PRT;
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01-NOV-1998
01-NOV-1998
01-MAR-2001
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01-MAY-2000
01-MAR-2001
RADA.
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                                                                                                     Pyrococcus furiosus.
Archaea; Euryarchaeota;
                                                                                                                         RADA.
                                                                                                                                 RECOMBINASE
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                                                                           SEQUENCE FROM
                                                                                             NCBI_TaxID=2261;
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 InterPro;
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 IPR000445; -.
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STRAIN-DSM 3638;
Diruggiero J., Brown J.R., Bo
"DNA repair systems in Archae
"DNA repair systems in Orchae
common ancestor.";
J. Mol. Evol. 0:0-0(1998).
EMBL; AF052597; AAC34998.1;
HSSP; P03017; 2REB.
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"The Rada protein from a hyperthermophilic archaeon Pyrobaculum islandicum is a DNA-dependent ATPase that shows two distinct modes ATP hydrolysis at temperatures above and below 75C.";

Submitted (APR-199) to the EMBL/GenBank/DDBJ databases.

EMBL; AB026115; BAA88984.1; -.

InterPro; IPR001553; -.

InterPro; IPR001553; -.

PRINTS; PR00142; RECA.

SMART; SM0382; AAA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 NAWDMFSDELSQKHITTGSGDLNDILGGGIHCKEVTEIGGVPGVGKTQLGIQLAINVQIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ERYAHLDKSPSLPVASAPYAVTGKGIRD 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLSLKLMKIAKTYNLAVVLLNQVTTKFTEGSF--QLTLALGDSWSHSCTNRLILHWN-GN
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                                                                       J.R., Bogert
in Archaea: Me
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16,
                                                                                                                                                                                   Thermococcales; Thermococcaceae;
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13,
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InterPro; IPR003593;
SMART; SM00382; AAA;
SEQUENCE 349 AA; 3
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Q9V233;
Q1-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      structure and evolution.";
Submitted (JUL-1999) to the
EMBL; AJ248283: CAB49165.1;
InterPro; IPR001553; -.
InterPro; IPR003593; -.
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NCBI_TaxID=29292;
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                                                                                                                                                                                       AGISEGAALKIIQAARKAANLGTFMRADEYLKKRESIGRISTGSKSLDKLLGGGIETQAI 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TEIGGVPGVGKTQLGIQLAINVQIPVECGGLGGKAVYIDTEGSFMVERVYQIAEGCIRDI 115
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                                           LEHFPHSHEKSSSVQKQLQPERFLADIYYFRICSYTEQIAVINYMEKFLRE----HKDVR
                                                                                       TEVFGEFGSGKTQLAHTLAVMVQLPPEEGGLNGSVIWIDTENTFRPERIREIAK-----
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(TrEMBLrel. 13, Last sequence up)
(TrEMBLrel. 16, Last annotation
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NRGLDPDEVLKHIYVARAFNSNHQMLLVQQAEDKIKELLNTDKPVK
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Pred. No.
                                                                                                                                                                                                                                                                                 Score 345; DB 1; I
Pred. No. 8.7e-21;
1; Mismatches 107;
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EMBL; AF198107; AAF74403.1; -
InterPro; IPR001553; -
InterPro; IPR003593; -
SMART; SM00382; AAA; 1.
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01-MAR-2001
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DMC1.
DMC1.
Cynops pyrrhogaster
Charvota; Metazoa;
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NCBI_TaxID=5741;
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Eukaryota; Diplomonadida; Hexamitidae;
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(TrEMBLrel. 15, Last sequence up)
(TrEMBLrel. 16, Last annotation)
                                                                                                                                                                                                                                                                                        PRELIMINARY;
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Chordata;
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Last sequence update)
Last annotation updat
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                 Craniata;
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ca; Vertebrata;
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                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1998 (TrEMBLrel.
01-AUG-1998 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
                                                                                                                                                                                                                                      McKean P.G., Benson F.E.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF062380; AAC16335.1; -.
                                                                                                                                                                                                                                                                                  STRAIN-FRIEDLIN;
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                                                                                                                                                                   SMART; SM00382; AAA; 1
SEQUENCE 364 AA; 39:
                                                                                                                                                                                              HSSP; P03017; 2REB.
InterPro; IPR001553; -.
InterPro; IPR003593; -.
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                          Eukaryota; Euglenozoa;
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             94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LARLQKISEEYNVAVFVTNQMTADPGAAMSFQADPKKPIGGHILAHASTTRISLRKGRGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLKIMKIAKTYNLAVVLLNQVTT-KFTEGSFQLTLAL---GDSWSHSCTNRLILH-WNGN 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YARAYTSEHQMELLDYVAAKFHEEAGIFKLLVIDSIMALFRVDFSGRGELAERQQKLAQM 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YFRICSYTEQIAVINYM-EKFLREHKDVRIVIIDSVTFHFRQDFE---DLALRTRVLSGL 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GYTGGKVIFIDTENTFRPDR------LRDIADRFSVDH------DAVLDNVL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EYSEKRKMVFHITTGSQEFDKLLGGGIESMAITETFGEFRTGKTQLSHTLCVTAQLPGTD 151
          DTEGSFMVERVYQIAEGCIRDILEHFPHSHEKSSSVQKQLQPERFLADIYYFRICSYTEQ 153
                                                                   ITTGSGDLNDIL-GGGIHCKEVTEIGGVPGVGKTQLGIQLAINVQIPVECGGLGGKAVYI 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ERYAHLDKSPSLPVASAPYAVTGKGIRDA 283
                                        ISTGSTALDQLLGGGGIESRSITEAFGEFRTGKTQIGHTLCVTCQLPLEMGGGNGKAVYV 185
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                                                                                                49;
                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation updat
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                                                                                                              Score 316; DB 5; Pred. No. 2.3e-18;
                                                                                                                                                                     A5475644CE8AFBE5 CRC64;
                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         364
                                                                                                                                                                                                                                                                                                                                          Trypanosomatidae; Leishmania
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Best Local Similarity
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044246;
044246;
01-JUN-1998
01-JUN-1998
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPRO03593; -.
InterPro; IPRO03593; -.
SMART; SM00382; AAA; 1.
340 AA; 37681 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9UH11 PRELIMINARY; PRT; 340 AA.
Q9UH11;
Q1-MAY-2000 (TIEMBLIEL. 13, Created)
Q1-MAY-2000 (TIEMBLIEL. 13, Last sequence update)
Q1-MAR-2001 (TIEMBLIEL. 16, Last annotation update)
Q1-MAR-2001 (TIEMBLIEL. 16, Last annotation update)
DJ199H16.1 (DMC1 (CDOSAGE SUPPRESSOR OF MCXI, YEAST HOMOLOG) MEIOSIS-
SPECIFIC HOMOLOGOUS RECOMBINATION PROTEIN (LIM15))).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             343
                                                                                                                                                                                                                                                                                              144 YFRICSYTEQIAVINYM-EKFLREHKDVRIVIIDSVTFHFRQDFE---DLALRTRVLSGL 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186 DTEGTFRPERIRPIAERFGMD------SNSV-----LDNILVARAYTHEHQ 225
                                                                                                                                            307
                                                                                                                                                                                                     250 LSRLQKISEEYNVAVFVTNQMT---ADPGATMTFQADPKKPIGGHILAHASTTRISLRKG
                                                                                                                                                                                                                                                                    190
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                                                                                                                                                                                                                                                                                                                                                                                           90 EYSEKRKMVFHITTGSQEFDKLLGGGIESMAITEAFGEFRTGKTQLSHTLCVTAQLPGAG 149
                                                                                              13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NLAVVLLNQVTTKFTEGSFQLTLA-----LGDSWSHSCTNRLILH-WNGNERYAHLDKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IAVINYMEKFLREHKDVRIVIIDSVTFHFRQDFE----DLALRTRVLSGLSLKLMKIAKTY 210
                                                                                                                                                                                                                                                                                                                                                            GGLGGKAVYIDTEGSFMVERVYQIAEGCIRDILEHFPHSHEKSSSVQKQLQPERFLADIY 143
                                                                                                                                                                                                                                                                                                                                                                                                                          ELSQK-----HITTGSGDLNDILGGGIHCKEVTEIGGVPGVGKTQLGIQLAINVQIPVEC 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PSLPELECVYSISEQGIIDAV 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSLPVASAPYAVTGKGIRDAV 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        {\tt NIAVYITNOVVS--DPGGASMFVADPKKPVGGHILAHASTTRLSLRKGRGDQRVCKIFDS}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AHLLSMVAAKMAEDQ-FSLLVVDSITALFRVDFSGRGELAERQQKLAKMLSQLIKIAEEF
                                                                                                                                                                                                                                  SLKLMKIAKTYNLAVVLLNQVTTKFTEGSFQLTLAL-----GDSWSHSCTNRLILH-W
                                                                                                                                                                                                                                                                    YARAYTSEHQMELLDYVAAKFHEEAGIFKLLIIDSIMALFRVDFSGRGELAERQQKLAQM
                                                                                                                                                                                                                                                                                                                                 GYPGGKIIFIDTENTFRPDR-----LRDIADRFNVDH
                                                                                                                                          RGELRIAKIYDSPEMPENEATFAITAGGIGDA 338
                                                                                                                                                                         NGNERYAHLDKSPSLPVASAPYAVTGKGIRDA 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; 68
 (TrEMBLrel.) (TrEMBLrel.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAB45656.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20.5%; Score 313; DB 4; 32.7%; Pred. No. 3.7e-18;
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    16,
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    Last sequence update)
Last annotation update)
                                  Created)
                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    040A6E4CF1FEBFA2 CRC64;
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                                                                  357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           40;
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8

RECA/RAD51/DMC1-LIKE PROTEIN

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01-OCT-2000 (TrEMBLrel. 15, C:
01-OCT-2000 (TrEMBLrel. 15, L:
01-MAR-2001 (TrEMBLrel. 16, I:
LIM15/DMC1 HOMOLOG PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                               Matches
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EMBL; AF061201; AAD10194.1; -
EMBL; AL023838; CAB61038.1; -
InterPro; IPR000445; -
InterPro; IPR001553; -
InterPro; IPR003583; -
Pfam; PF00633; HH; 1
SMART; SM00278; HhH1; 1
                                                                       Q9P972
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99077299; PubMed=9862483;
Rinaldo C., Ederle S., Rocco V., La Volpe A.;
"The Caenorhabditis elegans RAD51 homolog is transcribed into two
alternative mRNAs potentially encoding proteins of different sizes.";
Mol. Gen. Genet. 260:289-294(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 282:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Higashitani A., Sato Submitted (FEB-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans.
Eukaryota; Metazoa; Nemat.
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-99069613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted
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                                                                                                                                    337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               investigating biology
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                                                                                                                                                          266
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                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
nes 87; Conser
                                                                                                                                                                                                       LAVVLLNQVTTKFTEGS--FQLTLAL---GDSWSHSCTNRLILH-WNGNERYAHLDKSPS
                                                                                                                                  LPEAEATYSITNHGIEDA
                                                                                                                                                          LPVASAPYAVTGKGIRDA
                                                                                                                                                                                VAVIITNQVVAQVDGGASMFQADAKKPIGGHIIAHMSTTRLYLRKGKGENRVAKMVQSPN
                                                                                                                                                                                                                               ALTIRAGAMMSESR-YAVVIVDCATAHFRNEYTGRGDLAERQMKLSAFLKCLAKLADEYG
                                                                                                                                                                                                                                                      AVINYMEKFLREHKDVRIVIIDSVTFHFRQDFE---DLALRTRVLSGLSLKLMKIAKTYN
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                                                                                                                                                                                                                                                                                                     TEGSFMVERVYQIAEGCIRDILEHFPHSHEKSSSVQKQLQPERFLADIYYFRICSYTEQI
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                                                                                                                                                                                                                                                                                                                                                   ITTGSGDLNDILGGGIHCKEVTEIGGVPGVGKTQLGIQLAINVQIPVECGGLGGKAVYID 94
                                                                                                                                                                                                                                                                                                                                                                                                                                          SM00278;
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                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                          39193
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                                                                                                                                  354
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                                                                                                                                                                                                                                                                                                                                                                                                                                          , WM
                                                                                                                                                                                                                                                                                                                                                                              36;
                    Last sequence update)
Last annotation update)
                                             Created)
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                                                                                                                                                                                                                                                                                                                                                                            Score 309; DB 5;
Pred. No. 8.5e-18;
6; Mismatches 105
                                                                                                                                                                                                                                                                                                                                                                                                                                          ECED8C7021204BED CRC64;
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                                                                                                                                                                                                                                                                             -----RYNMDSAHVLENIAVARAYNSEHLM
                                                                       345
                                                                       A
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RESULT
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L Mol. Gen. Genet. 262:781-789(1999).
EMBL; AB036801; BAA89533.1; -...
InterPro; IPR001553; -...
InterPro; IPR003593; -...
PRINTS; PRO0142; RECA.
SMART; SM00382; AAA; 1...
SEQUENCE 3/6 xx.
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Best Local :
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001680;
01-JUL-1997
01-JUL-1997
01-MAR-2001
                 Submitted (MAR-1997) to tl
EMBL; U94994; AAB53331.1;
HSSP; P03017; 2REB.
InterPro; IPR001553; -.
                                                                                                                                                                                                                                                    Eukaryota; Metazoa; F
Pterygota; Neoptera;
                                                                                                                                    TISSUE=TESTIS;
                                                                                                                                                                                                                                 Bombycoidea; Bombycidae;
                                                                                                                                                                                                                                                                                                   Bombyx mori (Silk moth)
                                                                                                                                                                                                                                                                                                                                                    DMC1 HOMOLOG.
                                                                                                                Larsen
                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                        NCBI_TaxID=7091;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nara T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nara
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Coprinus cinereus (Inky cap fungus).
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Agaricales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20092483; PubMed=10628861;
Nara T., Saka T., Sawado T., Takase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    148 CSYTEQIAVINYMEKFLREHKDVRIVIIDSVTFHFRQDFE---DLALRTRVLSGLSLKLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108 ISTGSKLVDGILGGGVMSQSITEVYGEYRTGKTQLAHTMSVVAQLPPEYGGAAGKVAYID 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95 TEGSFMVERVYQIAEGCIRDILEHFPHSHEKSSSVQKQLQPERF-----LADIYYFRI 147
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Neoptera; Endopterygota; Lepidoptera;
                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel.
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16,
                                                                                     the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                   Bombyx.
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Pred. No. 2.3e
10; Mismatches
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ptera; Glossata;
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DR SMART; SM00382; AAA; 1.
SQ SEQUENCE 341 AA; 37773 MW; 303D4C9F67427F46 CRC64;
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Db	Qy	ф	Qy	Db	Qy	Db	Qy	Db	Qy	Que Bes Mat
295 AHASTTRISLRKGRGDNRIAKIYDSPDLPESBATFAITNGGVADA 339	240 SHSCTNRLILH-WNGNERYAHLDKSPSLPVASAPYAVTGKGIRDA 283	238 GELADROOKLAQVISRLOKISEEYNVAVFITNOMTADPGATLTFQADPKKPIGGNIL 294	188 -DLALRTRVLSGLSLKLMKIAKTYNLAVVLLNQVTTKFTEGSFQLTLALGDSW 239	179 -NLDQNAVLDNVLYARAYTSEHQAELLDYVAAKFHEEAGVFKLLIIDSIMALFRVDFSGR 237	131 KQLQPERFLADIYYFRICSYTEQIAVINYM-EKFLREHKDVRIVIIDSVTFHFRQDFE 187	138 HTLCVTTQIPNSKGYQGGKVMFLDTEHTFRPDRLRPIADRF 178	71 IQLAINVQIPVECGGLGGKAVYIDTEGSFMVERVYQIAEGCIRDILEHFPHSHEKSSSVQ 130	79 QKVVTLGFMTALEV-SDRRKQVFKISTGSTELDKLLAGGIESMAITEVFGEFRTGKTQLS 137	13 QKYVS-GAQNAWDMFSDELSQK-HITTGSGDLNDILGGGIHCKEVTEIGGVPGVGKTQLG 70	Query Match 19.7%; Score 302; DB 5; Length 341; Best Local Similarity 32.3%; Pred. No. 3.1e-17; Matches 92; Conservative 49; Mismatches 106; Indels 38; Gaps 10;

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